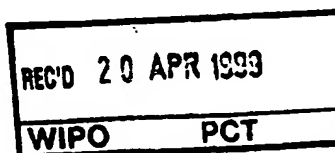


EXHIBIT A



PCT/AU99/00195



5

Patent Office
Canberra

I, KIM MARSHALL, MANAGER EXAMINATION SUPPORT AND SALES,
hereby certify that the annexed is a true copy of the Provisional specification in
connection with Application No. PP 2492 for a patent by AG-GENE AUSTRALIA
LTD and STATE OF QUEENSLAND THROUGH ITS DEPARTMENT OF
PRIMARY INDUSTRIES filed on 20 March 1998.

WITNESS my hand this Fourteenth
day of April 1999

KIM MARSHALL
MANAGER EXAMINATION SUPPORT AND
SALES



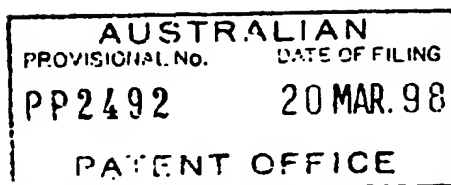
PRIORITY DOCUMENT

SUBMITTED OR TRANSMITTED IN
COMPLIANCE WITH RULE 17.1(a) OR (b)

Applicants : Michael Wayne Graham and
Robert Norman Rice
U.S. Serial No. : 10/759,841
Filed : January 15, 2004

Exhibit A

Regulation 3.2



Ag-Gene Australia Ltd

AND

State of Queensland through its Department of Primary Industries

A U S T R A L I A

Patents Act 1990

PROVISIONAL SPECIFICATION

for the invention entitled:

"Synthetic Genes and Genetic Constructs Comprising Same I"

The invention is described in the following statement:

- 1A -

SYNTHETIC GENES AND GENETIC CONSTRUCTS COMPRISING SAME I

FIELD OF THE INVENTION

5 The present invention relates generally to synthetic genes for modifying endogenous gene expression in a cell, tissue or organ of a transgenic organism, in particular a transgenic animal or plant. More particularly, the present invention provides novel synthetic genes and genetic constructs which are capable of repressing delaying or otherwise reducing the expression of an endogenous gene or a target gene in an organism when introduced thereto.

10

BACKGROUND TO THE INVENTION

Controlling metabolic pathways in eukaryotic organisms is desirable for the purposes of producing novel traits therein or introducing novel traits into a particular cell, tissue or organ
15 of said organism. Whilst recombinant DNA technology has provided significant progress in an understanding of the mechanisms regulating eukaryotic gene expression, much less progress has been made in the actual manipulation of gene expression to produce novel traits. Moreover, there are only limited means by which human intervention may lead to a repression, delay or reduction in eukaryotic gene expression.

20

Current methods for down-regulating gene expression using recombinant DNA technology comprise the introduction of a transgene to the cell which is capable of repressing expression of an endogenous target gene, either transcriptionally or post-transcriptionally. However, the precise mechanism is not known. Moreover, the efficiency of current approaches is low and
25 the results are variable and unpredictable.

Attempts to improve the accuracy and predictability of methods for regulating gene expression in cells, in particular the repression, delay or reduction in expression of viral target genes in eukaryotic cells, foreign transgenes or other foreign genes introduced into
30 cells, tissues or organs by natural means, or endogenous genes which are expressed to

- 2 -

produce undesirable traits for a particular purpose, have been largely unsuccessful possibly due to a lack of knowledge of the precise mechanisms involved. As a consequence, the efficiency of methods currently available remains low and highly variable.

5 In work leading up to the present invention, the inventors sought to elucidate the mechanisms involved in down-regulating gene expression in an attempt to provide improved methods therefor. In so doing the inventors have developed a wide range of synthetic genes capable of modulating gene expression in both prokaryotic and eukaryotic cells and genetic constructs comprising same.

10 Bibliographic details of the publications referred to by author in this specification are collected at the end of the description. Sequence identity numbers (SEQ ID NOs.) for the nucleotide and amino acid sequences referred to in the specification are defined after the bibliography.

15 Throughout this specification and the claims that follow, unless the context requires otherwise, the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element or integer or group of elements or integers but not the exclusion of any other element or integer or group of elements or
20 integers.

As used herein, the term "derived from" shall be taken to indicate that a particular integer or group of integers has originated from the species specified, but has not necessarily been obtained directly from the specified source.

25

SUMMARY OF THE INVENTION

The present invention provides novel synthetic genes and improved genetic constructs comprising same for modifying endogenous or target gene expression in cells, tissues and/or
30 organs which are either transfected or stably transformed therewith.

- 3 -

Accordingly, one aspect of the present invention provides a synthetic gene which is capable of modifying target gene expression in a cell, tissue or organ of a prokaryotic or eukaryotic organism which is transfected or transformed therewith, wherein said synthetic gene at least comprises a structural gene sequence comprising a nucleotide sequence which is substantially identical to the nucleotide sequence of said target gene or a derivative thereof or a complementary sequence thereto placed operably under the control of a promoter sequence which is operable in said cell, tissue or organ.

A further aspect of the invention provides a synthetic gene which is capable of modifying the expression of a target gene in a cell, tissue or organ of a prokaryotic or eukaryotic organism which is transfected or transformed therewith, wherein said synthetic gene at least comprises multiple structural gene sequences, wherein each of said structural gene sequences comprises a nucleotide sequence which is substantially identical to the nucleotide sequence of said target gene or a derivative thereof or a complementary sequence thereto and wherein said multiple structural gene sequences are placed operably under the control of a single promoter sequence which is operable in said cell, tissue or organ.

A third aspect of the present invention provides a synthetic gene which is capable of modifying the expression of a target gene in a cell, tissue or organ of a prokaryote or eukaryote which is transfected or transformed therewith wherein said synthetic gene at least comprises multiple structural gene sequences wherein each of said structural gene sequences is placed operably under the control of a promoter sequence which is operable in said cell, tissue or organ and wherein each of said structural gene sequences comprises a nucleotide sequence which is substantially identical to the nucleotide sequence of said target gene or a derivative thereof or a complementary sequence thereto.

A further aspect of the present invention provides a genetic construct which is capable of modifying the expression of an endogenous gene or target gene in a transformed or transfected cell, tissue or organ wherein said genetic construct at least comprises the synthetic gene of the invention and one or more origins of replication and/or selectable marker gene

- 4 -

sequences.

A still further aspect of the invention provides a cell, tissue, organ or organism comprising the synthetic genes and genetic constructs described herein.

5

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a copy of a diagrammatic representation of the plasmid pEGFP-N1 MCS.

10 Figure 2 is a copy of a diagrammatic representation of the plasmid pCMV.cass.

Figure 3 is a copy of a diagrammatic representation of the plasmid pCR.Bgl-GFP-Bam.

Figure 4 is a copy of a diagrammatic representation of the plasmid pCR.SV40L.

15

Figure 5 is a copy of a diagrammatic representation of the plasmid pCMV.SV40L.cass.

Figure 6 is a copy of a diagrammatic representation of the plasmid pCR.BEV.1.

20 Figure 7 is a copy of a diagrammatic representation of the plasmid pCR.BEV.2.

Figure 8 is a copy of a diagrammatic representation of the plasmid pCR.BEV.3.

Figure 9 is a copy of a diagrammatic representation of the plasmid pEGFP.BEV.1.

25

Figure 10 is a copy of a diagrammatic representation of the plasmid pCMV.BEV.2.

Figure 11 is a copy of a diagrammatic representation of the plasmid pCMV.VEB.

30 Figure 12 is a copy of a diagrammatic representation of the plasmid pCMV.BEVnt.

- 5 -

Figure 13 is a copy of a diagrammatic representation of the plasmid pCMV.BEVx2.

Figure 14 is a copy of a diagrammatic representation of the plasmid pCMV.BEV.VEB.

5 Figure 15 is a copy of a diagrammatic representation of the plasmid pCMV.BEV.GFP.VEB.

Figure 16 is a copy of a diagrammatic representation of the plasmid pCMV.BEV.SV40L-0.

10 Figure 17 is a copy of a diagrammatic representation of the plasmid pCMV.0.SV40L.BEV.

Figure 18 is a copy of a diagrammatic representation of the plasmid pCMV.0.SV40L.VEB.

Figure 19 is a copy of a diagrammatic representation of the plasmid pCMV.BEV.SV40L.BEV.

15

Figure 20 is a copy of a diagrammatic representation of the plasmid pCMV.BEV.SV40L.VEB.

Figure 21 is a copy of a diagrammatic representation of the plasmid pCMV.SV40LR.cass.

20

Figure 22 is a copy of a diagrammatic representation of the plasmid pCMV.BEV.SV40LR.

Figure 23 is a copy of a diagrammatic representation of the plasmid pCMV.TYR.

25 Figure 24 is a copy of a diagrammatic representation of the plasmid pCMV.TYRLIB.

Figure 25 is a copy of a diagrammatic representation of the plasmid pCMV.Lac.

30 Figure 26 is a copy of a diagrammatic representation of the plasmid pCMVLacI.OPRSV1.cass.

- 6 -

Figure 27 is a copy of a diagrammatic representation of the plasmid pCMVLacI.OPRSV1.GFP.cass.

Figure 28 is a copy of a diagrammatic representation of the plasmid
5 pCMVLacI.TYR.OPRSV1.GFP.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

- 10 One aspect of the present invention provides a synthetic gene which is capable of modifying the expression of a target gene in a cell, tissue or organ wherein said synthetic gene at least comprises a structural gene comprising a nucleotide sequence which is substantially identical to the nucleotide sequence of said target gene or a derivative thereof or a complementary sequence thereto placed operably under the control of a promoter which is operable in said
15 cell, tissue or organ.

Reference herein to a "gene" is to be taken in its broadest context and includes:

- (i) a classical genomic gene consisting of transcriptional and/or translational regulatory sequences and/or a coding region and/or non-translated sequences (i.e. introns, 5'- and 3'- untranslated sequences);
- 20 (ii) mRNA or cDNA corresponding to the coding regions (i.e. exons) optionally comprising 5'- or 3'-untranslated sequences linked thereto; or
- (iii) an amplified DNA fragment or other recombinant nucleic acid molecule produced *in vitro* and comprising all or a part of the coding region and/or 5'- or 3'-
25 untranslated sequences linked thereto.

The term "gene" is also used to describe synthetic or fusion molecules encoding all or part of a functional product, in particular a sense or antisense mRNA product or a peptide, oligopeptide or polypeptide or a biologically-active protein.

30

- 7 -

The term "synthetic gene" refers to a non-naturally occurring gene as hereinbefore defined which preferably comprises at least one or more transcriptional and/or translational regulatory sequences operably linked to a structural gene sequence.

- 5 The term "structural gene" shall be taken to refer to a nucleotide sequence which is capable of being transmitted to produce mRNA and optionally, encodes a peptide, oligopeptide, polypeptide or biologically active protein molecule. Those skilled in the art will be aware that not all mRNA is capable of being translated into a peptide, oligopeptide, polypeptide or protein, for example if the mRNA lacks a functional translation start signal or alternatively,
- 10 if the mRNA is antisense mRNA. The present invention clearly encompasses synthetic genes comprising nucleotide sequences which are not capable of encoding peptides, oligopeptides, polypeptides or biologically-active proteins. In particular, the present inventors have found that such synthetic genes may be advantageous in modifying target gene expression in cells, tissues or organs of a prokaryotic or eukaryotic organism.

15

- The term "target gene" shall be taken to refer to any gene, the expression of which is to be modified using the synthetic gene of the invention. Preferred target genes include, but are not limited to viral genes and foreign genes which have been introduced into the cell, tissue
- 20 or organ or alternatively, genes which are endogenous to the cell, tissue or organ.

- Wherein the target gene is a viral gene, it is particularly preferred that the viral gene encodes a function which is essential for replication or reproduction of the virus, such as but not limited to a DNA polymerase or RNA polymerase gene or a viral coat protein gene, amongst
- 25 others. In a particularly preferred embodiment, the target gene comprises an RNA polymerase gene derived from a single-stranded (+) RNA virus such as bovine enterovirus (BEV), Sinbis alphavirus or a lentivirus such as, but not limited to, an immunodeficiency virus (eg. HIV-1) or alternatively, a DNA polymerase derived from a double-stranded DNA virus such as bovine herpesvirus or herpes simplex virus I (HSV1), amongst others.

30

- 8 -

Wherein the target gene is a foreign gene, those skilled in the art will be aware that it will have been introduced to the cell, tissue or organ using transformation technology or alternatively, comprise a gene derived from a pathogen which has been introduced to said cell, tissue or organ by naturally-occurring gene transfer processes.

5

Particularly preferred foreign target genes include any transgene which has been introduced to the cell, tissue or organ.

Wherein the target gene is a gene which is endogenous to the cell, tissue or organ, it is
10 particular preferred that its expression is capable of being monitored by a visual assay, enzyme assay or immunoassay. Particularly preferred endogenous target genes are those detected by visual assay means.

The synthetic genes of the present invention may be derived from naturally-occurring genes
15 by standard recombinant techniques, the only requirement being that the synthetic gene is substantially identical at the nucleotide sequence level to at least a part of the target gene, the expression of which is to be modified. By "substantially identical" is meant that the structural gene sequence of the synthetic gene is at least about 80% - 90% identical to 30 or more contiguous nucleotides of the target gene, more preferably at least about 90-95% identical to
20 30 or more contiguous nucleotides of the target gene and even more preferably at least about 95-99% identical or absolutely identical to 30 or ore contiguous nucleotides of the target gene.

Generally, a gene of the invention may be subjected to mutagenesis to produce single or
25 multiple nucleotide substitutions, deletions and/or additions without affecting its ability to modify target gene expression. Nucleotide insertional derivatives of the synthetic gene of the present invention include 5' and 3' terminal fusions as well as intra-sequence insertions of single or multiple nucleotides. Insertional nucleotide sequence variants are those in which one or more nucleotides are introduced into a predetermined site in the nucleotide sequence
30 although random insertion is also possible with suitable screening of the resulting product.

- 9 -

Deletional variants are characterised by the removal of one or more nucleotides from the sequence. Substitutional nucleotide variants are those in which at least one nucleotide in the sequence has been removed and a different nucleotide inserted in its place. Such a substitution may be "silent" in that the substitution does not change the amino acid defined
5 by the codon. Alternatively, substituents are designed to alter one amino acid for another similar acting amino acid, or amino acid of like charge, polarity, or hydrophobicity.

Accordingly, the present invention extends to homologues, analogues and derivatives of the synthetic genes described herein.

10

For the present purpose, "homologues" of a gene as hereinbefore defined or of a nucleotide sequence shall be taken to refer to an isolated nucleic acid molecule which is substantially the same as the nucleic acid molecule of the present invention or its complementary nucleotide sequence, notwithstanding the occurrence within said sequence, of one or more nucleotide
15 substitutions, insertions, deletions, or rearrangements.

"Analogues" of a gene as hereinbefore defined or of a nucleotide sequence set forth herein shall be taken to refer to an isolated nucleic acid molecule which is substantially the same as a nucleic acid molecule of the present invention or its complementary nucleotide sequence,
20 notwithstanding the occurrence of any non-nucleotide constituents not normally present in said isolated nucleic acid molecule, for example carbohydrates, radiochemicals including radionucleotides, reporter molecules such as, but not limited to DIG, alkaline phosphatase or horseradish peroxidase, amongst others.

"Derivatives" of a gene as hereinbefore defined or of a nucleotide sequence set forth herein shall be taken to refer to any isolated nucleic acid molecule which contains significant sequence similarity to said sequence or a part thereof. Generally, the nucleotide sequence of the present invention may be subjected to mutagenesis to produce single or multiple nucleotide substitutions, deletions and/or insertions. Nucleotide insertional derivatives of the
30 nucleotide sequence of the present invention include 5' and 3' terminal fusions as well as

- 10 -

intra-sequence insertions of single or multiple nucleotides or nucleotide analogues. Insertional nucleotide sequence variants are those in which one or more nucleotides or nucleotide analogues are introduced into a predetermined site in the nucleotide sequence of said sequence, although random insertion is also possible with suitable screening of the
5 resulting product being performed. Deletional variants are characterised by the removal of one or more nucleotides from the nucleotide sequence. Substitutional nucleotide variants are those in which at least one nucleotide in the sequence has been removed and a different nucleotide or nucleotide analogue inserted in its place.

- 10 Accordingly, the structural gene component of the synthetic gene may comprise a nucleotide sequence which is at least about 80% identical to at least about 30 contiguous nucleotides of an endogenous target gene, a foreign target gene or a viral target gene present in a cell, tissue or organ or a homologue, analogue, derivative thereof or a complementary sequence thereto.
- 15 Preferred structural gene components of the synthetic gene of the invention comprise at least about 20-30 nucleotides in length derived from a viral DNA polymerase, viral RNA polymerase, viral coat protein or visually-detectable gene, more particularly an RNA polymerase gene derived from a virus selected from the list comprising BEV, Sindbis alphavirus, HIV-1, bovine herpes virus and HSV1 or a visually-detectable gene which is
20 involved in determining pigmentation, cell death or other external phenotype on a cell, tissue, organ or organism, amongst others.

In a particularly preferred embodiment, the structural gene component of the synthetic gene comprises at least about 20-30 nucleotides in length derived from the BEV RNA-dependent
25 RNA polymerase gene or the murine tyrosinase gene or the *Escherichia coli lac* repressor gene *lacI* or a complementary sequence thereto.

The structural gene component may comprise a nucleotide sequence which encodes an amino acid sequence, with or without a translation start signal (ATG) or a nucleotide sequence
30 which is complementary thereto. Those skilled in the art will be aware that, in the absence

- 11 -

of the translation start signal in an appropriate reading frame, the mRNA encoded by the structural gene will not be translated in most eukaryotic and prokaryotic cells.

Alternatively, the structural gene may comprise a nucleotide sequence which does not encode
5 an amino acid sequence or more commonly, comprises one or more open reading frames
which encode one or more peptides, oligopeptides or polypeptides which are unrelated at the
amino acid sequence level to the amino acid sequence encoded by the target gene. For
example, the mRNA product of the structural gene may be inserted into the synthetic gene
of the invention so as to alter or disrupt the reading frame of the structural gene and produce
10 one or more frame shift mutations in the translation product thereof relative to the translation
product encoded by the target gene, notwithstanding a substantial identity between the
structural gene and the target gene on the one hand and the corresponding mRNA products
of the structural gene and the target gene on the other hand. Such effects may be produced
by introducing one or two nucleotide substitutions or deletions into the structural gene,
15 relative to the target gene sequence or alternatively, by introducing a translation start codon
5'-ATG-3' upstream of any nucleotide in the structural gene which occurs at a particular
position in a codon of the corresponding target gene such that the position of said nucleotide
in the codon of the structural gene is altered.

20 Alternatively, the structural gene may encode no amino acid sequence or one or more amino
acid sequences which are unrelated to the amino acid sequence encoded by the target gene
wherein said structural gene is transcribed in the antisense orientation from the synthetic gene
promoter, relative to the direction of transcription of the corresponding target gene. In such
circumstances, the mRNA product of the structural gene will comprise a nucleotide sequence
25 which is complementary to the nucleotide sequence in the corresponding region of the mRNA
encoded by the target gene.

The present invention clearly encompasses synthetic genes wherein the structural gene
component is operably connected in the sense or antisense orientation to a promoter sequence
30 and irrespective of the capacity of said structural gene to encode an amino acid sequence

- 12 -

which is encoded by the target gene. Accordingly, the structural gene component may further comprise 5'-untranslated region and/or 3'-untranslated region and/or intron (eg. SV40 intron) and/or a coding region derived from the target gene or a complementary nucleotide sequence thereto.

5

Reference herein to a "promoter" is to be taken in its broadest context and includes the transcriptional regulatory sequences of a classical genomic gene, including the TATA box which is required for accurate transcription initiation in eukaryotic cells, with or without a CCAAT box sequence and additional regulatory elements (i.e. upstream activating sequences, enhancers and silencers). For expression in prokaryotic cells, such as bacteria, the promoter should at least contain the -35 box and -10 box sequences.

A promoter is usually, but not necessarily, positioned upstream or 5', of the structural gene component of the synthetic gene of the invention, the expression of which it regulates. Furthermore, the regulatory elements comprising a promoter are usually positioned within 2 kb of the start site of transcription of the structural gene.

In the present context, the term "promoter" is also used to describe a synthetic or fusion molecule, or derivative which confers, activates or enhances expression of an isolated nucleic acid molecule, in a cell, such as a plant, animal, insect, fungal, yeast or bacterial cell. Preferred promoters may contain additional copies of one or more specific regulatory elements, to further enhance expression of a structural gene which expression it regulates and/or to alter the spatial expression and/or temporal expression of same. For example, regulatory elements which confer inducibility on the expression of the structural gene may be placed adjacent to a heterologous promoter sequence driving expression of a nucleic acid molecule.

Placing a structural gene under the regulatory control of a promoter sequence means positioning said molecule such that expression is controlled by the promoter sequence. Promoters are generally positioned 5' (upstream) to the genes that they control. In the

- 13 -

construction of heterologous promoter/structural gene combinations it is generally preferred to position the promoter at a distance from the gene transcription start site that is approximately the same as the distance between that promoter and the gene it controls in its natural setting, i.e., the gene from which the promoter is derived. As is known in the art, some variation in this distance can be accommodated without loss of promoter function. Similarly, the preferred positioning of a regulatory sequence element with respect to a heterologous gene to be placed under its control is defined by the positioning of the element in its natural setting, i.e., the genes from which it is derived. Again, as is known in the art, some variation in this distance can also occur.

10

Examples of promoters suitable for use in the synthetic genes of the present invention include viral, fungal, bacterial, animal and plant derived promoters capable of functioning in plant, animal, insect, fungal, yeast or bacterial cells. The promoter may regulate the expression of the structural gene component constitutively, or differentially with respect to cell, the tissue or organ in which expression occurs or, with respect to the developmental stage at which expression occurs, or in response to external stimuli such as physiological stresses, or pathogens, or metal ions, amongst others.

Preferably, the promoter is capable of regulating expression of a nucleic acid molecule in a eukaryotic cell, tissue or organ, at least during the period of time over which the target gene is expressed therein and more preferably also immediately preceding the commencement of detectable expression of the target gene in said cell, tissue or organ.

Accordingly, strong constitutive promoters are particularly preferred for the purposes of the present invention or promoters which may be induced by virus infection or the commencement of target gene expression.

Examples of preferred promoters include the bacteriophage T7 promoter, bacteriophage T3 promoter, SP6 promoter, *lac* operator-promoter, *tac* promoter, SV40 late promoter, SV40 early promoter, RSV-LTR promoter, CMV IE promoter and the like.

30

- 14 -

Particularly preferred promoters contemplated herein include promoters operable in eukaryotic cells, for example the SV40 early promoter, SV40 late promoter or the CMV IE promoter sequence. Those skilled in the art will readily be aware of additional promoter sequences other than those specifically described.

5

In the present context, the terms "in operable connection with" or "operably under the control" or similar shall be taken to indicate that expression of the structural gene is under the control of the promoter sequence with which it is spatially connected; in a cell, tissue, organ or whole organism.

10

In a more particularly preferred embodiment of the invention, the synthetic gene according to this aspect of the invention comprises the coding region of the BEV polymerase gene placed in the sense orientation operably under the control of the CMV IE promoter or SV40 late promoter. In an alternative embodiment, the synthetic gene comprises a nucleotide
15 sequence derived from the coding region of the BEV polymerase gene but lacking a translation - start site, placed in the sense orientation in operable connection with the CMV IE promoter or SV40 late promoter. In a further alternative embodiment, the synthetic gene comprises a nucleotide sequence derived from the BEV polymerase gene placed in the antisense orientation relative to the BEV polymerase gene and in operable connection with
20 the CMV IE promoter or the SV40 late promoter sequence.

For the present purposes, the term "BEV polymerase" as used herein shall be taken to refer to a structural gene, cDNA molecule, genomic gene or nucleotide sequence at least about 30-50 nucleotides in length which is derived from the nucleotide sequence of the bovine
25 enterovirus(BEV) RNA-dependent RNA polymerase gene, including both translatable and non-translatable nucleotide sequences and nucleotide sequences which are complementary to a part of the nucleotide sequence of the full-length BEV RNA-dependent RNA polymerase gene.

30 In a further alternative embodiment, the synthetic gene according to this aspect of the

- 15 -

invention comprises the coding region of a tyrosinase gene, in particular the murine tyrosinase gene, placed in the sense orientation operably under the control of the CMV IE promoter or SV40 late promoter. As with other embodiments described herein, the synthetic gene (i.e. tyrosinase gene) may lack a functional translation start site or be introduced in the
5 antisense orientation. The present invention clearly encompasses all such embodiments.

As used herein, the term "tyrosinase gene" shall be taken to refer to a structural gene, cDNA molecule, genomic gene or nucleotide sequence which is capable of encoding the tyrosinase enzyme or a polypeptide fragment thereof or alternatively, a nucleotide sequence which is
10 complementary to said structural gene, cDNA molecule, genomic gene or nucleotide sequence. Particularly preferred tyrosinase genes for use in the performance of the present invention include, but are not limited to, those described by Kwon *et al* (1988) and homologues, analogues and derivatives thereof and complementary nucleotide sequences thereto.

15

In still a further alternative embodiment, the synthetic gene according to this aspect of the invention comprises the coding region of the *lacI* gene, placed in the sense orientation operably under the control of the CMV IE promoter or SV40 late promoter. As with other
20 embodiments described herein, the synthetic gene (i.e. *E. coli lacI* gene) may lack a functional translation start site or be introduced in the antisense orientation. The present invention clearly encompasses all such embodiments.

As used herein, the term "*lacI* gene" shall be taken to refer to a structural gene, cDNA molecule, genomic gene or nucleotide sequence which is capable of encoding a polypeptide
25 repressor of the *lacZ* gene which encodes the enzyme β -galactosidase or alternatively, a nucleotide sequence which is complementary to said structural gene, cDNA molecule, genomic gene or nucleotide sequence. Those skilled in the art will be aware that the *lac* repressor is a DNA-binding protein which acts on the *lac* operator-promoter sequence. In the presence of one of a variety of β -galactosides, the affinity of the *lac* repressor for the *lac*
30 operator-promoter sequence is lowered, thereby allowing RNA polymerase to bind the *lac*

- 16 -

operator-promoter region to activate transcription of the *lac* operon.

Standard methods may be used to produce the structural genes of the present invention, in particular the BEV polymerase and tyrosinase genes which are derived from publicly available material. For example, the BEV polymerase and tyrosinase genes may be amplified using the polymerase chain reaction or alternatively, isolated using standard hybridisation techniques known to those skilled in the art.

For the purposes of nomenclature, the nucleotide sequence of the cDNA encoding murine tyrosinase is publicly available under GenBank Accession No. M20234.

10

A second aspect of the present invention provides a synthetic gene which is capable of modifying the expression of a target gene in a cell, tissue or organ, wherein said synthetic gene at least comprises multiple structural gene sequences wherein each of said structural gene sequences comprises a nucleotide sequence which is substantially identical to the nucleotide sequence of the target gene or a derivative thereof or a complementary sequence thereto and wherein said multiple structural gene sequences are placed operably under the control of a single promoter sequence which is operable in said cell, tissue or organ.

20 As used herein, the term "multiple structural gene sequences" or similar term shall be taken to refer to any number of structural genes as defined herein which is greater than or equal to two. Accordingly, a multiple structural gene sequence may comprise a tandem repeat or concatemer of two or more identical nucleotide sequences or alternatively, a tandem array or concatemer of non-identical nucleotide sequences, the only requirement being that each of the structural gene sequences contained therein is substantially identical to the target gene sequence or a complementary sequence thereto. In this regard, those skilled in the art will be aware that a cDNA molecule may also be regarded as a multiple structural gene sequence in the context of the present invention, in so far as it comprises a tandem array or concatemer of exon sequences derived from a genomic target gene. Accordingly, cDNA molecules and any tandem array, tandem repeat or concatemer of exon sequences and/or intron sequences

25
30

- 17 -

and/or 5'-untranslated and/or 3'-untranslated sequences are clearly encompassed by this embodiment of the invention.

Preferably, the multiple structural gene comprises at least 2-4 individual structural gene sequences, more preferably at least about 4-6 individual structural gene sequences and more preferably at least about 6-8 individual structural gene sequences.

The optimum number of structural gene sequences which may be involved in the synthetic gene of the present invention will vary considerably, depending upon the length of each of said structural gene sequences, their orientation and degree of identity to each other. For example, those skilled in the art will be aware of the inherent instability of palindromic nucleotide sequences *in vivo* and the difficulties associated with constructing long synthetic genes comprising inverted repeated nucleotide sequences, because of the tendency for such sequences to form hairpin loops and to recombine *in vivo*. Notwithstanding such difficulties, the optimum number of structural gene sequences to be included in the synthetic genes of the present invention may be determined empirically by those skilled in the art, without any undue experimentation and by following standard procedures such as the construction of the synthetic gene of the invention using recombinase-deficient cell lines, reducing the number of repeated sequences to a level which eliminates or minimises recombination events and by keeping the total length of the multiple structural gene sequence to an acceptable limit, preferably no more than 5-10kb, more preferably no more than 2-5kb and even more preferably no more than 0.5-2.0kb in length.

In an alternative embodiment, each structural gene contained within the multiple structural gene unit of the subject synthetic gene may comprise a nucleotide sequence which is substantially identical to a different target gene in the same organism. Such an arrangement may be of particular utility when the synthetic gene is intended to provide protection against a pathogen in a cell, tissue or organ, in particular a viral pathogen, by modifying the expression of viral target genes. For example, the multiple structural gene may comprise nucleotide sequences which are substantially identical to two or more target genes selected

- 18 -

from the list comprising DNA polymerase, RNA polymerase and coat protein or other target gene which is essential for viral infectivity, replication or reproduction. However, it is preferred with this arrangement that the structural gene units are selected such that the target genes to which they are substantially identical are normally expressed at approximately the same time (or later) in an infected cell, tissue or organ as (than) the multiple structural gene of the subject synthetic gene is expressed under control of the promoter sequence. This means that the promoter controlling expression of the multiple structural gene will usually be selected to confer expression in the cell, tissue or organ over the entire life cycle of the virus when the viral target genes are expressed at different stages of infection.

10

The individual structural gene units of the multiple structural gene according to the embodiments described herein may be spatially connected in any orientation relative to each other, for example head-to-head, head-to-tail or tail-to-tail and all such configurations are within the scope of the invention.

15

Preferably, the multiple structural gene unit comprises two structural genes in a head-to-tail or head-to-head configuration. More preferably, the multiple structural gene unit comprises two identical or substantially identical structural genes or a homologue, analogue or derivative thereof in a head-to-tail configuration as a direct repeat or alternatively, in a head-to-head

20 configuration as an inverted repeat or palindrome.

In a particularly preferred embodiment, the multiple structural gene unit comprises two identical or substantially identical structural genes comprising nucleotide sequences derived from the BEV polymerase or tyrosinase gene or a homologue, analogue or derivative thereof, placed in a head-to-head or head-to-tail configuration.

25

According to this aspect of the invention, wherein the multiple structural gene or any individual structural gene unit thereof is intended to be both transcribed and translated, a translation start signal may be included at the 5' end of that open reading frame. In a particularly preferred embodiment, the structural gene unit which is positioned nearer the 5'

30

- 19 -

end of the synthetic gene comprises an in-frame translation start signal of facilitate translation of the first open reading frame of the multiple structural gene in a cell, tissue or organ into which the synthetic gene is introduced. Those skilled in the art will be aware that it is also possible to produce a fusion polypeptide from such an arrangement provided that the
5 individual structural gene units are positioned such that their open reading frames are in-frame with respect to each other or alternatively, the individual structural gene units are separated by intron/exon splice boundary sequences such that splicing of the mRNA product of the synthetic gene produces a translatable mRNA wherein the said open reading frames are in-frame with respect to each other. Such embodiments are clearly contemplated by the
10 present invention. Intron/exon splice junction sequences are well-known in the art and the skilled person would readily be able to introduce such sequences to the 5'- and 3'- ends of a structural gene unit of the synthetic genes described herein.

The individual structural genes comprising the multiple structural gene unit may be further
15 spatially separated by the addition of a linker molecule or "stuffer fragment" there between. The stuffer fragment may comprise any combination of nucleotide or amino acid residues, carbohydrate molecules or oligosaccharide molecules or carbon atoms or a homologue, analogue or derivative thereof which is capable of being linked covalently to a nucleic acid molecule.

20

Preferably, embodiment, the stuffer fragment comprises a sequence of nucleotides or a homologue, analogue or derivative thereof.

More preferably, the stuffer fragment comprises a sequence of nucleotides of at least about
25 10-50 nucleotides in length, even more preferably at least about 50-100 nucleotides in length and still more preferably at least about 100-500 nucleotides in length.

Wherein the multiple structural gene unit comprises intron/exon splice junction sequences, the stuffer fragment may serve as an intron sequence placed between the 3'-splice site of the
30 structural gene nearer the 5'-end of the gene and the 5'- splice site of the next downstream

- 20 -

structural gene. Alternatively, wherein it is desirable for more than two adjacent structural genes to be translated, the stuffer fragment placed there between should not include an in-frame translation stop codon, absent intron/exon splice junction sequences at both ends of the stuffer fragment or the addition of a translation start codon at the 5' end of each structural
5 gene unit, as will be obvious to those skilled in the art.

Preferred stuffer fragments are those which encode detectable marker proteins or biologically-active analogues and derivatives thereof, for example luciferase, β -galacturonase, β -galactosidase, chloramphenicol acetyltransferase or green fluorescent protein, amongst others.

10

According to this embodiment, the detectable marker or an analogue or derivative thereof serves to indicate the expression of the synthetic gene of the invention in a cell, tissue or organ by virtue of its ability to confer a specific detectable phenotype thereon, preferably a visually-detectable phenotype.

15

In a more particularly preferred embodiment of the invention, the multiple structural gene comprises an interrupted direct repeat or interrupted palindrome comprising two identical or substantially-identical BEV polymerase structural gene sequences or alternatively, two identical or substantially-identical tyrosinase structural gene sequences or a homologue,
20 analogue or derivative thereof separated by a stuffer fragment comprising a nucleotide sequence which encodes green-fluorescent protein or a biologically-active analogue or derivative thereof.

As used herein, the term "green fluorescent protein" or "GFP" shall be taken to refer to a
25 protein, polypeptide or peptide which is capable of producing a strong green fluorescence when excited with near ultraviolet radiation or blue light or a homologue, analogue or derivative thereof. Accordingly, the term "GFP gene" shall be taken to refer to a nucleotide sequence which is capable of encoding GFP or a complementary nucleotide sequence thereto. Particularly preferred GFPs and GFP genes according to the present invention are derived
30 from the jellyfish *Aequoria victoria* as described by Prasher *et al* (1992) or in International

- 21 -

Patent Publication No. WO 95/07463, amongst others.

A further aspect of the invention provides for each structural gene of the multiple structural gene unit to be placed operably under the control of a separate promoter sequence.

5

According to this embodiment, the promoters controlling expression of the structural gene unit are preferably different promoter sequences, to reduce competition there between for cellular transcription factors and RNA polymerases. Preferred promoters are selected from those referred to *supra*.

10

Those skilled in the art will know how to modify the arrangement or configuration of the individual structural genes as described *supra* to regulate their expression from separate promoter sequences.

- 15 In a particularly preferred embodiment, the multiple structural gene unit comprises two or more BEV polymerase structural genes or two or more tyrosinase structural genes wherein each of said structural genes is placed operably in connection with a different promoter sequence. More particularly preferred, the multiple structural gene unit comprises two BEV polymerase structural genes or two tyrosinase structural genes positioned as inverted repeats
- 20 or direct repeats wherein one of said structural genes is placed operably in connection with the CMV IE promoter. Even more preferably, at least one of the BEV polymerase structural genes or tyrosinase genes comprising the multiple structural gene is presented in the sense orientation and comprises a translation start signal to facilitate translation of mRNA encoded therefrom.

25

Those skilled in the art will be aware that the structural genes comprising the multiple structural gene unit according to this aspect of the invention are expressed as physically-distinct mRNA species and, as a consequence, wherein said mRNA species are translated, no fusion polypeptide will be produced there between. However, the present invention clearly

30 extends to synthetic gene which comprises two or more structural genes operably connected

- 22 -

to a first promoter sequence and one or more structural genes operably connected to one or more additional promoter sequences.

The synthetic genes described *supra* are capable of being modified further, for example by the inclusion of marker nucleotide sequences encoding a detectable marker enzyme or a functional analogue or derivative thereof, to facilitate detection of the synthetic gene in a cell, tissue or organ in which it is expressed. According to this embodiment, the marker nucleotide sequences will be present in a translatable format and expressed, for example as a fusion polypeptide with the translation product(s) of any one or more of the structural genes or alternatively as a non-fusion polypeptide.

Alternatively or in addition, the synthetic genes described *supra* may further comprise one or more transcription termination sequences placed at the 3'-end of the transcriptional unit of the synthetic gene sequence.

15

The term "terminator" refers to a DNA sequence at the end of a transcriptional unit which signals termination of transcription. Terminators are 3'-non-translated DNA sequences containing a polyadenylation signal, which facilitates the addition of polyadenylate sequences to the 3'-end of a primary transcript. Terminators active in cells derived from viruses, yeasts, moulds, bacteria, insects, birds, mammals and plants are known and described in the literature. They may be isolated from bacteria, fungi, viruses, animals and/or plants.

Examples of terminators particularly suitable for use in the synthetic genes of the present invention include the SV40 polyadenylation signal, the HSV TK polyadenylation signal, the CYC1 terminator, ADH terminator, SPA terminator, nopaline synthase (NOS) gene terminator of *Agrobacterium tumefaciens*, the terminator of the Cauliflower mosaic virus (CaMV) 35S gene, the *zein* gene terminator from *Zea mays*, the Rubisco small subunit gene (SSU) gene terminator sequences, subclover stunt virus (SCSV) gene sequence terminators, any *rho*-independent *E.coli* terminator, or the *lacZ* alpha terminator, amongst others.

30

- 23 -

In a particularly preferred embodiment, the terminator is the SV40 polyadenylation signal or the HSV TK polyadenylation signal which are operable in animal cells, tissues and organs or the *lacZ* alpha terminator which is active in prokaryotic cells.

- 5 Those skilled in the art will be aware of additional promoter sequences and terminator sequences which may be suitable for use in performing the invention. Such sequences may readily be used without any undue experimentation.

- The synthetic genes of the present invention may be introduced to a suitable cell, tissue or
10 organ without modification as linear DNA in the form of a genetic construct, optionally contained within a suitable carrier, such as a cell, virus particle or liposome, amongst others. To produce a genetic construct, the synthetic gene of the invention is inserted into a suitable vector or episome molecule, such as a bacteriophage vector, viral vector or a plasmid, cosmid or artificial chromosome vector which is capable of being maintained and/or replicated and/or
15 expressed in the host cell, tissue or organ into which it is subsequently introduced.

Accordingly a further aspect of the invention provides a genetic construct which at least comprises the synthetic gene according to any one or more of the embodiments described herein and one or more origins of replication and/or selectable marker gene sequences.

20

Usually, an origin of replication or a selectable marker gene suitable for use in bacteria is physically-separated from those genetic sequences contained in the genetic construct which are intended to be expressed or transferred to a eukaryotic cell, or integrated into the genome of a eukaryotic cell.

25

In a particularly preferred embodiment, the origin of replication is functional in a bacterial cell and comprises the pUC or the ColE1 origin or alternatively the origin of replication is operable in a eukaryotic cell, tissue and more preferably comprises the 2 micron (2 μ m) origin of replication or the SV40 origin of replication.

30

- 24 -

As used herein, the term "selectable marker gene" includes any gene which confers a phenotype on a cell in which it is expressed to facilitate the identification and/or selection of cells which are transfected or transformed with a genetic construct of the invention or a derivative thereof.

5

Suitable selectable marker genes contemplated herein include the ampicillin-resistance gene (Amp^r), tetracycline-resistance gene (Tc^r), bacterial kanamycin-resistance gene (Kan^r), is the zeocin resistance gene (Zeocin is a drug of bleomycin family which is trademark of InVitrogen Corporation), the *AURI-C* gene which confers resistance to the antibiotic aureobasidin A, phosphinothricin-resistance gene, neomycin phosphotransferase gene (*nptII*), hygromycin-resistance gene, β -glucuronidase (GUS) gene, chloramphenicol acetyltransferase (CAT) gene, green fluorescent protein- encoding gene or the luciferase gene, amongst others.

10
15 Preferably, the selectable marker gene is the *nptII* gene or Kan^r gene or green fluorescent protein (GFP)-encoding gene.

Those skilled in the art will be aware of other selectable marker genes useful in the performance of the present invention and the subject invention is not limited by the nature of the selectable marker gene.

20

The present invention extends to all genetic constructs essentially as defined herein, which include further genetic sequences intended for the maintenance and/or replication of said genetic construct in prokaryotes and/or the integration of said genetic construct or a part thereof into the genome of a eukaryotic cell or organism.

25

The present invention further extends to an isolated cell, tissue or organ comprising the synthetic gene described herein or a genetic construct comprising same. Any standard means may be used for their introduction including cell mating, transformation or transfection procedures known to those skilled in the art or described by Ausubel *et al.* (1992).

30

- 25 -

The present invention is further described by reference to the following non-limiting Examples.

5

EXAMPLE 1

Base Plasmids

Plasmid pEGFP-N1 MCS

- 10 Plasmid pEGFP-N1 MCS (Figure 1; Clontech) contains the CMV IE promoter operably connected to an open reading frame encoding a red-shifted variant of wild-type green fluorescent protein (GFP; Prasher *et al.*, 1992; Chalfie *et al.*, 1994; Inouye and Tsuji, 1994), which has been optimised for brighter fluorescence. The specific GFP variant encoded by pEGFP-N1 MCS has been disclosed by Cormack *et al.* (1996). Plasmid pEGFP-N1 MCS
- 15 contains a multiple cloning site comprising *Bgl*II and *Bam*HI sites and many other restriction endonuclease cleavage sites, located between the CMV IE promoter and the GFP open reading frame. Structural genes cloned into the multiple cloning site will be expressed at the transcriptional level if they lack a functional translation start site, however such structural gene sequences will not be expressed at the protein level (i.e. translated). Structural gene
- 20 sequences inserted into the multiple cloning site which comprise a functional translation start site will be expressed as GFP fusion polypeptides if they are cloned in-frame with the GFP-encoding sequence. The plasmid further comprises an SV40 polyadenylation signal downstream of the GFP open reading frame to direct proper processing of the 3'-end of mRNA transcribed from the CMV-IE promoter sequence. The plasmid further comprises the
- 25 SV40 origin of replication functional in animal cells; the neomycin-resistance gene comprising SV40 early promoter (SV40 EP in Figure 1) operably connected to the neomycin/kanamycin-resistance gene derived from Tn5 (Kan/neo in Figure 1) and the HSV thymidine kinase polyadenylation signal (HSV TK poly (A) in Figure 1), for selection of transformed cells on kamanycin, neomycin or G418; the pUC19 origin of replication which
- 30 is functional in bacterial cells (pUC Ori in Figure 1); and the fl origin of replication for

- 26 -

single-stranded DNA production (fl Ori in Figure 1).

pCMVLacI

- 5 Plasmid pCMVLacI is a commercially-obtainable mammalian expression vector (Stratagene) comprising the *lacI* gene encoding the *lac* repressor and a gene coding for hygromycin resistance (Hyg^r).

Plasmid pOPRSV1/MCS

10

Plasmid pOPRSV1/MCS is a commercially-obtainable mammalian expression vector (Stratagene), comprising the OPRSV1 promoter sequence (a modified RSV-LTR promoter), SV40 intron sequence, *lac* operator sequence, multiple cloning site and thymidine kinase (TK) gene transcription terminator sequence [i.e. TK poly(A) signal].

15

Plasmid pSVL

- Plasmid pSVL is commercially-obtainable from Pharmacia and serves as a source of the SV40 late promoter sequence. The nucleotide sequence of pSVL is also publicly available as
20 GenBank Accession Number U13868.

Plasmid pCMV.cass

- Plasmid pCMV.cass (Figure 2) is an expression cassette for driving expression of a structural
25 gene sequence under control of the CMV-IE promoter sequence. Plasmid pCMV.cass was derived from pEGFP-N1 MCS by deletion of the GFP open reading frame as follows: Plasmid pEGFP-N1 MCS was digested with *Pin*AI and *Not* I, blunt-ended using *Pfu*I polymerase and then re-ligated. Structural gene sequences are cloned into pCMV.cass using the multiple cloning site, which is identical to the multiple cloning site of pEGFP-N1 MCS,
30 except it lacks the *Pin*AI site.

- 27 -

Plasmid pCR2.1

Plasmid pCR2.1 is commercially available from Stratagene and comprises the lacZ promoter sequence and *lacZ-α* transcription terminator, with a cloning site for the insertion of structural gene sequences there between. Plasmid pCR2.1 is designed to clone nucleic acid fragments by virtue of the A-overhang frequently synthesized by *Taq* polymerase during the polymerase chain reaction. The plasmid further comprises the ColE1 and f1 origins of replication and kanamycin-resistance and ampicillin-resistance genes.

10 Plasmid pCR.Bgl-GFP-Bam

Plasmid pCR.Bgl-GFP-Bam (Figure 3) comprises an internal region of the GFP open reading frame derived from plasmid pEGFP-N1 MCS (Figure 1) placed operably under the control of the lacZ promoter. To produce this plasmid, a region of the GFP open reading frame was amplified from pEGFP-N1 MCS using the amplification primers Bgl-GFP (SEQ ID NO:5) and GFP-Bam (SEQ ID NO:6) and cloned into plasmid pCR2.1. The internal GFP-encoding region in plasmid pCR.Bgl-GFP-Bam lacks functional translational start and stop codons.

Plasmid pCR.SV40L

20

Plasmid pCR.SV40L (Figure 4) comprises the SV40 late promoter derived from plasmid pSVL (GenBank Accession No. U13868; Pharmacia), cloned into pCR2.1 (Stratagene). To produce this plasmid, the SV40 late promoter was amplified using the primers SV40-1 (SEQ ID NO:7) and SV40-2 (SEQ ID NO:8) which comprise *Sal* I cloning sites to facilitate sub-cloning of the amplified DNA fragment into pCMV.cass. SEQ ID No. 7 also contains a synthetic poly (A) site at the 5' end, such that the amplification product comprises the synthetic poly(A) site at the 5' end of the SV40 promoter sequence.

- 28 -

Plasmid pCMV.SV40L.cass

Plasmid pCMV.SV40L.cass (Figure 5) comprises the synthetic poly A site and the SV40 late promoter sequence from plasmid pCR.SV40L (Figure 4), sub-cloned as a *Sal* I fragment, into the *Sal* I site of plasmid pCMV.cass (Figure 2), such that the CMV-IE promoter and SV40 late promoter sequences are capable of directing transcription in the same direction. Accordingly, the synthetic poly(A) site at the 5' end of the SV40 promoter sequence is used as a transcription terminator for structural genes expressed from the CMV IE promoter in this plasmid, which also provides for the insertion of said structural gene via the multiple cloning site present between the SV40 late promoter and the synthetic poly(A) site (Figure 5). The multiple cloning sites are located behind the CMV-IE and SV40 late promoters, including *Bam*HI and *Bgl*II sites.

EXAMPLE 2

BEV Polymerase-containing genes

Plasmid pCR.BEV.1

The BEV RNA-dependent RNA polymerase coding region was amplified as a 1,385 bp DNA fragment from a full-length cDNA clone encoding same, using the primers designated BEV-1 (SEQ ID NO:1) and BEV-2 (SEQ ID NO:2), under standard amplification conditions. The amplified DNA contained a 5'-*Bgl* II restriction enzyme site, derived from the BEV-1 primer sequence and a 3'-*Bam*HI restriction enzyme site, derived from the BEV-2 primer sequence. Additionally, as the BEV-1 primer sequence contains a translation start signal 5'-ATG-3' engineered at positions 15-17 of SEQ ID NO:1, the amplified BEV polymerase structural gene comprises the start site in-frame with BEV polymerase-encoding nucleotide sequences. Thus, the amplified BEV polymerase structural gene comprises the ATG start codon immediately upstream (ie. juxtaposed) to the BEV polymerase-encoding sequence. There is no translation stop codon in the amplified DNA.

- 29 -

The amplified BEV polymerase structural gene was cloned into plasmid pCR2.1 to produce pCR.BEV.1 (Figure 6).

Plasmid pCR.BEV.2

5

The complete BEV polymerase coding region was amplified from a full-length cDNA clone encoding same, using primers BEV-1 (SEQ ID NO:1) and BEV-3 (SEQ ID NO:3). Primer BEV-3 comprises a *Bam*HI restriction enzyme site at positions 5 to 10 inclusive of SEQ ID NO:3 and the complement of a translation stop signal at positions 11 to 13 of SEQ ID NO:3.

10 As a consequence, an open reading frame comprising a translation start signal and translation stop signal, contained between the *Bgl* II and *Bam*HI restriction sites. The amplified fragment was cloned into pCR2.1 to produce plasmid pCR2.BEV.2 (Figure 7).

Plasmid pCR.BEV.3

15

A non-translatable BEV polymerase structural gene was amplified from a full-length BEV polymerase cDNA clone using the amplification primers BEV-3 (SEQ ID NO:3) and BEV-4 (SEQ ID NO:4). Primer BEV-4 comprises a *Bgl*II cloning site at positions 5-10 of SEQ ID NO:4 and sequences downstream of this *Bgl*II site are homologous to nucleotide sequences

20 of the BEV polymerase gene. There is no functional ATG start codon in the amplified DNA product of primers BEV-3 and BEV-4. The BEV polymerase is expressed as part of a polyprotein and, as a consequence, there is no ATG translation start site in this gene. The amplified DNA was cloned into plasmid pCR2.1 to yield plasmid pCR.BEV.3 (Figure 8).

25

- 30 -

EXAMPLE 3

Synthetic genes comprising a BEV polymerase structural gene
operably connected to the CMV-IE promoter sequence

5 Plasmid pEGFP.BEV.1

Plasmid pEGFP.BEV.1 (Figure 9) is capable of expressing the BEV polymerase structural gene as a GFP fusion polypeptide under the control of the CMV-IE promoter sequence. To produce plasmid pEGFP.BEV.1, the BEV polymerase sequence from pCR.BEV.1 (Figure 6) was cloned as a *Bgl*II-to-*Bam*HI fragment into *Bgl*II/*Bam*HI-digested pEGFP-N1 MCS (Figure 1).

Plasmid pCMV.BEV.2

15 Plasmid pCMV.BEV.2 (Figure 10) is capable of expressing the entire BEV polymerase open reading frame under the control of CMV-IE promoter sequence. To produce pCMV.BEV.2, the BEV polymerase sequence from pCR.BEV.2 (Figure 7) was sub-cloned in the sense orientation as a *Bgl*II-to-*Bam*HI fragment into *Bgl*II/*Bam*HI-digested pCMV.cass (Figure 2).

20 Plasmid pCMV.VEB

Plasmid pCMV.VEB (Figure 11) expresses an antisense BEV polymerase mRNA under the control of the CMV-IE promoter sequence. To produce plasmid pCMV.VEB, the BEV polymerase sequence from pCR.BEV.2 (Figure 7) was sub-cloned in the antisense orientation 25 as a *Bgl*II-to-*Bam*HI fragment into *Bgl*II/*Bam*HI-digested pCMV.cass (Figure 2).

Plasmid pCMV.BEVnt

Plasmid pCMV.BEVnt (Figure 12) expresses a non-translatable BEV polymerase structural 30 gene in the sense orientation under the control of the CMV-IE promoter sequence. To

- 31 -

produce pCMV.BEVnt, the BEV polymerase sequence from pCR.BEV.3 (Figure 8) was sub-cloned in the sense orientation as a *Bgl*II-to-*Bam*HI fragment into *Bgl*II/*Bam*HI-digested pCMV.cass (Figure 2).

5 Plasmid pCMV.BEVx2

Plasmid pCMV.BEVx2 (Figure 13) comprises a direct repeat of a complete BEV polymerase open reading frame under the control of the CMV-IE promoter sequence. In eukaryotic cells at least, the open reading frame located nearer the CMV-IE promoter is translatable. To produce pCMV.BEVx2, the BEV polymerase structural gene from plasmid pCR.BEV.2 (Figure 7) was sub-cloned in the sense orientation as a *Bgl*II-to-*Bam*HI fragment into *Bam*HI-digested pCMV.BEV.2 (Figure 10), immediately downstream of the BEV polymerase structural gene already present therein.

15 Plasmid pCMV.BEV.VEB

Plasmid pCMV.BEV.VEB (Figure 14) comprises an inverted repeat or palindrome of a complete BEV polymerase open reading frame under the control of the CMV-IE promoter sequence. In eukaryotic cells at least, the open reading frame located nearer the CMV-IE promoter is translatable. To produce pCMV.BEV.VEB, the BEV polymerase structural gene from plasmid pCR.BEV.2 (Figure 7) was sub-cloned in the antisense orientation as a *Bgl*II-to-*Bam*HI fragment into *Bam*HI-digested pCMV.BEV.2 (Figure 10), immediately downstream of the BEV polymerase structural gene already present therein.

25 Plasmid pCMV.BEV.GFP.VEB

Plasmid pCMV.BEV.GFP.VEB (Figure 15) is similar to plasmid pCMV.BEV.VEB except that the BEV structural gene inverted repeat or palindrome is interrupted by the insertion of a GFP open reading frame (stuffer fragment) therein. To produce plasmid pCMV.BEV.GFP.VEB, the GFP stuffer fragment from pCR.Bgl-GFP-Bam (Figure 3) was

- 32 -

first sub-cloned in the sense orientation as a *Bgl*II-to-*Bam*HI fragment into *Bam*HI-digested pCMV.BEV.2 (Figure 7) to produce an intermediate plasmid pCMV.BEV.GFP wherein the BEV polymerase-encoding and GFP-encoding sequences are contained within the same 5'-*Bgl*II-to-*Bam*HI-3' fragment. The BEV polymerase structural gene from pCMV.BEV.2 (Figure 7) was then cloned in the antisense orientation as a *Bgl*II-to-*Bam*HI fragment into *Bam*HI-digested pCMV.BEV.GFP. The BEV polymerase structural gene nearer the CMV-IE promoter sequence in plasmid pCMV.BEV.GFP.VEB is capable of being translated, at least in eukaryotic cells.

10 **EXAMPLE 4**

Synthetic genes comprising BEV polymerase structural genes operably connected to multiple promoter sequences

Plasmid pCMV.BEV.SV40L-O

15

Plasmid pCMV.BEV.SV40L-O (Figure 16) comprises a translatable BEV polymerase structural gene derived from plasmid pCR.BEV.2 (Figure 7) inserted in the sense orientation between the CMV-IE promoter and the SV40 late promoter sequences of plasmid pCMV.SV40L.cass (Figure 5). To produce plasmid pCMV.BEV.SV40L-O, the BEV polymerase structural gene was sub-cloned as a *Bgl*II-to-*Bam*HI fragment into *Bgl*II-digested pCMV.SV40L.cass DNA.

Plasmid pCMV.O.SV40L.BEV

25 Plasmid pCMV.O.SV40L.BEV (Figure 17) comprises a translatable BEV polymerase structural gene derived from plasmid pCR.BEV.2 (Figure 7) cloned downstream of tandem CMV-IE promoter and SV40 late promoter sequences present in plasmid pCMV.SV40L.cass (Figure 5). To produce plasmid pCMV.O.SV40L.BEV, the BEV polymerase structural gene was sub-cloned in the sense orientation as a *Bgl*II-to-*Bam*HI fragment into *Bam*HI-digested pCMV.SV40L.cass DNA.

30

Plasmid pCMV.O.SV40L.VEB

Plasmid pCMV.O.SV40L.VEB (Figure 18) comprises an antisense BEV polymerase structural gene derived from plasmid pCR.BEV.2 (Figure 7) cloned downstream of tandem CMV-IE promoter and SV40 late promoter sequences present in plasmid pCMV.SV40L.cass (Figure 5). To produce plasmid pCMV.O.SV40L.VEB, the BEV polymerase structural gene was sub-cloned in the antisense orientation as a *Bgl*III-to-*Bam*HI fragment into *Bam*HI-digested pCMV.SV40L.cass DNA.

10 Plasmid pCMV.BEV.SV40L.BEV

Plasmid pCMV.BEV.SV40L.BEV (Figure 19) comprises a multiple structural gene unit comprising two BEV polymerase structural genes placed operably and separately under control of the CMV-IE promoter and SV40 late promoter sequences. To produce plasmid pCMV.BEV.SV40L.BEV, the translatable BEV polymerase structural gene present in pCR.BEV.2 (Figure 7) was sub-cloned in the sense orientation as a *Bgl*III-to-*Bam*HI fragment behind the SV40 late promoter sequence present in *Bam*HI-digested pCMV.BEV.SV40L-O (Figure 16).

Plasmid pCMV.BEV.SV40L.VEB

20

Plasmid pCMV.BEV.SV40L.VEB (Figure 20) comprises a multiple structural gene unit comprising two BEV polymerase structural genes placed operably and separately under control of the CMV-IE promoter and SV40 late promoter sequences. To produce plasmid pCMV.BEV.SV40L.VEB, the translatable BEV polymerase structural gene present in pCR.BEV.2 (Figure 7) was sub-cloned in the antisense orientation as a *Bgl*III-to-*Bam*HI fragment behind the SV40 late promoter sequence present in *Bam*HI-digested pCMV.BEV.SV40L-O (Figure 16). In this plasmid, the BEV polymerase structural gene is expressed in the sense orientation under control of the CMV-IE promoter to produce a translatable mRNA, whilst the BEV polymerase structural gene is also expressed under control of the SV40 promoter to produce an antisense mRNA species.

Plasmid pCMV.SV40LR.cass

Plasmid pCMV.SV40LR.cass (Figure 21) comprises the SV40 late promoter sequence derived from plasmid pCR.SV40L (Figure 4), sub-cloned as a *SaII* fragment into the *SaII* site of the plasmid pCMV.cass (Figure 2), such that the CMV-IE or the SV40 late promoter may drive transcription of a structural gene or a multiple structural gene unit, in the sense or antisense orientation, as desired. A multiple cloning site is positioned between the opposing CMV-IE and SV40 late promoter sequences in this plasmid to facilitate the introduction of a structural gene sequence. In order for expression of a structural gene sequence to occur from this plasmid, it must be introduced with its own transcription termination sequence located at the 3' end, because there are no transcription termination sequences located between the opposing CMV-IE and SV40 late promoter sequences in this plasmid. Preferably, the structural gene sequence or multiple structural gene unit which is to be introduced into pCMV.SV40LR.cass will comprise both a 5' and a 3' polyadenylation signal as follows:

- 15 (i) where the structural gene sequence or multiple structural gene unit is to be expressed in the sense orientation from the CMV IE promoter sequence and/or in the antisense orientation from the SV40 late promoter, the 5' polyadenylation signal will be in the antisense orientation and the 3' polyadenylation signal will be in the sense orientation; and
- 20 (ii) where the structural gene sequence or multiple structural gene unit is to be expressed in the antisense orientation from the CMV IE promoter sequence and/or in the sense orientation from the SV40 late promoter, the 5' polyadenylation signal will be in the sense orientation and the 3' polyadenylation signal will be in the antisense orientation.

25

Alternatively or in addition, suitably-oriented terminator sequences may be placed at the 5'-end of the CMV and SV40L promoters, as shown in Figure 21.

Alternatively, plasmid pCMV.SV40LR.cass is further modified to produce a derivative plasmid which comprises two polyadenylation signals located between the CMV IE and SV40

30

- 35 -

late promoter sequences, in appropriate orientations to facilitate expression of any structural gene located therebetween in the sense or antisense orientation from either the CMV IE promoter or the SV40 promoter sequence. The present invention clearly encompasses such derivatives.

5

Plasmid pCMV.BEV.SV40LR

Plasmid pCMV.BEV.SV40LR (Figure 22) comprises a structural gene comprising the entire BEV polymerase open reading frame placed operably and separately under control of
10 opposing CMV-IE promoter and SV40 late promoter sequences, thereby potentially producing BEV polymerase transcripts at least from both strands of the full-length BEV polymerase structural gene. To produce plasmid pCMV.BEV.SV40LR, the translatable BEV polymerase structural gene present in pCR.BEV.2 (Figure 7) was sub-cloned, as a *Bgl*II-to-*Bam*HI fragment, into the unique *Bgl*II site of plasmid pCMV.SV40LR.cass (Figure 21), such
15 that the BEV open reading frame is present in the sense orientation relative to the CMV-IE promoter sequence.

Those skilled in the art will recognise that it is possible to generate a plasmid wherein the BEV polymerase fragment from pCR.BEV.2 is inserted in the antisense orientation, relative
20 to the CMV IE promoter sequence, using this cloning strategy. The present invention further encompasses such a genetic construct.

EXAMPLE 5

Synthetic genes and genetic constructs comprising the 25 tyrosinase open reading frame

Isolation of the tyrosinase open reading frame

The tyrosinase structural gene is isolated by polymerase chain reaction, from mRNA derived
30 from murine cells, using the following oligonucleotide primers under standard polymerase

- 36 -

chain reaction conditions:

Tyr 5' (forward primer; SEQ ID NO:9):

5'-CCCGGGGCTTAGTGTAACAGGCTGAGAG-3'; and

5 Tyr 3' (reverse primer; SEQ ID NO:10):

5'-CCCGGGCAAATCCCAGTCATTCTTAGAAAC-3'.

Nucleotide residues 1 to 6 in each primer represent a *SmaI* cloning site. Nucleotides 7 to 30 of primer Tyr 5' correspond to the 5'-end of the murine tyrosinase cDNA sequence disclosed in GenBank Accession No. M20234 (Kwon *et al*, 1988). Nucleotides 7 to 31 of primer Tyr 3' correspond to the complement of the nucleotide sequence of the 3'-end of the murine tyrosinase cDNA sequence.

Plasmid pCR.tyr

15

Plasmid pCR.tyr is produced by sub-cloning the amplified tyrosinase structural gene into plasmid pCR2.1 (Example 1), substantially according to the manufacturer's protocol. Plasmid pCR.tyr can be used as a base plasmid to produce a range of genetic constructs designed to express the tyrosinase structural gene or a multiple structural gene unit comprising same, under the control of one or more promoter sequences.

Plasmid pCMV.TYR

Plasmid pCMV.TYR (Figure 23) comprises the complete mouse tyrosinase cDNA sequence placed operably in connection, in the sense orientation, with the CMV-IE promoter sequence and upstream of the SV40 polyadenylation sequence. To produce pCMV.TYR, the full-length mouse tyrosinase cDNA sequence was excised from plasmid pCR.tyr by digestion with *SmaI* and then ligated, into the *SmaI* cloning site of pCMV.cass (Figure 2). Clones possessing the tyrosinase structural gene in the sense orientation relative to the CMV-IE promoter were then selected.

- 37 -

Plasmid pCMV.TYRLIB

Plasmid pCMV.TYRLIB (Figure 24) comprises a structural gene or multiple structural gene unit which comprises one or more tyrosinase gene fragments of 100 to 200 base pairs in length each, placed operably in connection with the CMV-IE promoter sequence and upstream of the SV40 polyadenylation signal. To produce pCMV.TYRLIB, blunt-ended fragments of the tyrosinase gene are ligated into *Sma*I-digested, dephosphorylated plasmid pCMV.cass DNA (Figure 2). The tyrosinase gene fragments are produced, for example, by sonication or mechanical shearing and end-repair using T4 DNA polymerase. Accordingly, the structural gene insert in plasmid pCMV.TYRLIB is variable and an representative library of pCMV.TYRLIB plasmids, covering the complete tyrosinase gene sequence, may be produced using such procedures. The present invention clearly encompasses such representative libraries. Those skilled in the art will recognise that such procedures are also useful for structural genes other than tyrosinase and, as a consequence, the present invention clearly extends to synthetic genes and genetic constructs wherein the structural gene present in pCMV.TYRLIB is a structural gene other than a tyrosinase gene fragment.

EXAMPLE 6

**Synthetic genes and genetic constructs comprising the
lacI open reading frame**

Plasmid pCMV.Lac

Plasmid pCMV.Lac (Figure 25) contains a CMV IE promoter driving expression of the lac repressor protein encoded by the *Escherichia coli lacI* gene. Accordingly, the open reading frame of the *LacI* gene is cloned in the sense orientation with respect to the CMV IE promoter sequence in this plasmid. This construct also contains the selectable marker for neomycin resistance.

30

- 38 -

To produce plasmid pCMV.Lac, the *lacI* gene was excised from plasmid pCMV.LacI (Stratagene) by digestion with *HindIII* and *BsaBI* and then ligated, in the sense orientation, into the multiple cloning site (MCS) of plasmid pCMV.cass (Figure 2) which had been digested with *HindIII* and *SmaI*.

5

Plasmid pCMVLacI.OPRSV1.cass

Plasmid pCMVLacI.OPRSV1.cass (Figure 26) is a dual expression construct in which the CMV-IE promoter drives expression of the *LacI* structural gene to produce the lac repressor
10 protein and the OPRSVI promoter drives the expression of a second structural gene or multiple structural gene unit placed operably under control of lac repressor protein.

To produce plasmid pCMVLac.OPRSV1.cass, a DNA fragment comprising the OPRSVI promoter, SV40 intron, *lac* operator sequence, multiple cloning site (MCS) and TK poly(A)
15 sequence was excised from plasmid pOPRSVI/MCS (Stratagene), by digestion with *SnaBI* and *AseI* restriction enzymes, then end-filled using *PfuI* polymerase and ligated into the end-filled *BglII* cloning site of plasmid pCMVLacI (Stratagene).

EXAMPLE 7

20

Synthetic genes and genetic constructs comprising the *lacI* and green fluorescent protein (GFP) open reading frames

Plasmid pCMVLacI.OPRSV1.GFP.cass

25 Plasmid pCMVLacI.OPRSV1.GFP.cass (Figure 27) is designed such that a structural gene or multiple structural gene unit can be fused to the 3' untranslated region of the *lacI* gene, by cloning directly into the unique *BsaBI* cloning site which is located after the *lacI* stop codon and before an SV40 polyadenylation signal. Alternatively, the *BS4B1* site may be modified to facilitate cloning, for example by the addition of linkers or adaptors. This construct also
30 contains the antibiotic selectable marker for hygromycin resistance.

- 39 -

To produce plasmid pCMVLacI.OPRSVI.GFP.cass, the enhanced GFP coding sequence was excised from plasmid pEGFP-N1 MCS (Figure 1) by digestion with *XhoI* and *NotI* and the DNA fragment thus produced was ligated into the *XhoI* and *NotI* cloning sites of the multiple cloning site present in plasmid pCMVLacI.OPRSVI.cass (Figure 26).

5

EXAMPLE 8

**Synthetic genes and genetic constructs comprising the
lacI and green fluorescent protein (GFP) and tyrosinase open reading frames**

Plasmid pCMVLacI.TYR.OPRSV1.GFP

10

Plasmid pCMVLacI.TYR.OPRSV1.GFP (Figure 28) is a dual construct in which the CMV IE promoter drives expression of the *lacI* gene and the mRNA of the mouse tyrosinase cDNA or a fragment thereof, whilst the OPRSVI promoter drives expression of GFP operably under control of the *lacI* gene. The construct is designed such that the mouse tyrosinase gene is fused 15 to the 3' untranslated region of the *lacI* gene via a unique *BsaB1* cloning site. This cloning site is located after the stop codon of the *lacI* coding sequence, but before the SV40 polyadenylation signal. The construct also contains the hygromycin-resistance gene as a selection marker.

To produce plasmid pCMVLacI.TYR.OPRSV1.GFP, the complete tyrosinase gene present in 20 plasmid pCR.tyr (Stratagene; Example 1) is isolated from host cells, digested with *SmaI* and ligated into *BsaB1*-digested and dephosphorylated plasmid pCMVLacI.OPRSVI.GFP.cass DNA (Figure 27).

- 40 -

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANT: AgGene Australia Pty.Ltd and The Government of Queensland as represented by Queensland Department of Primary Industries

10

ii) TITLE OF INVENTION: Synthetic genes and genetic constructs comprising same I

iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

15

(A) ADDRESSEE: DAVIES COLLISON CAVE

(B) STREET: 1 LITTLE COLLINS STREET

(C) CITY: MELBOURNE

(D) STATE: VICTORIA

(E) COUNTRY: AUSTRALIA

20

(F) ZIP: 3000

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

25

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: AU provisional

30

(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: HUGHES EL, JOHN E L

35

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: +61 3 9254 2777

(B) TELEFAX: +61 3 9254 2770

(C) TELEX: AA 31787

40

- 41 -

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGCAGATCT AACAAATGGCA GGACAAATCG AGTACATC

15 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCCGGGATCC TCGAAAGAAT CGTACCACTT C

31

(2) INFORMATION FOR SEQ ID NO:3:

30

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

40

- 42 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGCGGATCC TTAGAAAGAA TCGTACCAC

29

5 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGCAGATCT GGACAAATCG AGTACATC

28

(2) INFORMATION FOR SEQ ID NO:5:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

25 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

30

AGATCTGTAA ACGGCCACAA GTTCAG

26

(2) INFORMATION FOR SEQ ID NO:6:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

40

- 43 -

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

5 GGATCCTTGT ACAGCTCGTC CATGCC

26

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTCGACAATA AAATATCTTT ATTTTCATTA CATCTGTGTG TTGGTTTTTT GTGTGATTTT

60

20

TGCAAAAGCC TAGG

74

(2) INFORMATION FOR SEQ ID NO:8:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

35 GTCGACGTTT AGAGCAGAAG TAACACTTCC G

31

- 44 -

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCCGGGGCTT AGTGTAAC AGGCTGAGAG

15

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCCGGGCAAA TCCAGTCAT TTCTAGAAA C

31

30

- 45 -

EQUIVALENTS

Those skilled in the art will appreciate that the invention described herein is susceptible to variations and modifications other than those specifically described. It is to be understood
5 that the invention includes all such variations and modifications. The invention also includes all of the steps, features, compositions and compounds referred to or indicated in this specification, individually or collectively, and any and all combinations of any two or more of said steps or features.

10

REFERENCES

1. Ausubel, F.M. *et al.* (1987) *In: Current Protocols in Molecular Biology*, Wiley Interscience (ISBN 047140338).
- 15 2. Chalfie, M. *et al* (1994) *Science* 263: 802-805.
3. Cormack, B. *et al* (1996) *Gene* 173: 33-38.
- 20 4. Inouye, S. and Tsuji, F.I. (1994) *FEBS Letts.* 341: 277-280.
5. Kwon, B.S. *et al.* (1988) *Biochem. Biophys. Res. Comm.* 153:1301- 1309.
6. Prasher, D.C. *et al.* (1992) *Gene* 111: 229-233.

25

DATED this 19TH day of MARCH, 1998

Ag-Gene Australia Ltd AND

State of Queensland through its Department of Primary Industries

by DAVIES COLLISON CAVE

30 Patent Attorneys for the Applicants

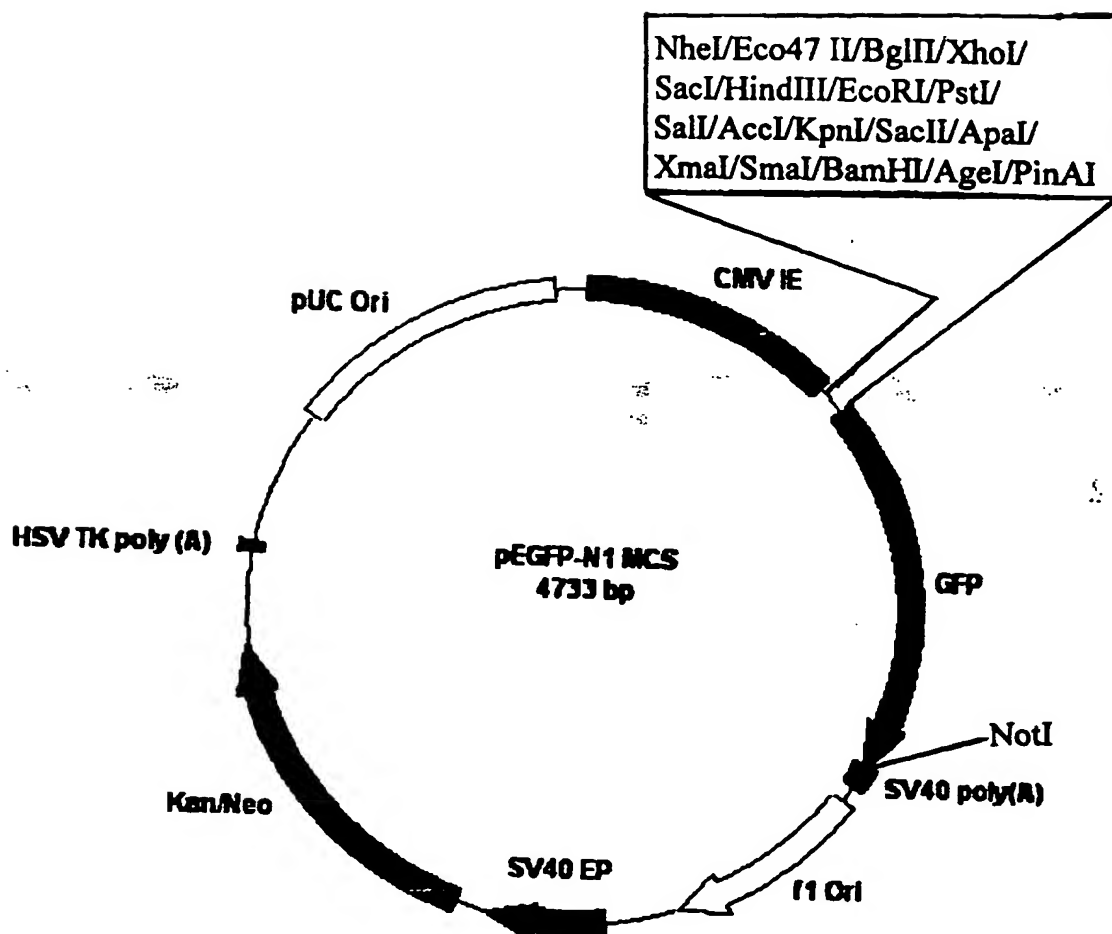


FIGURE 1

2/28

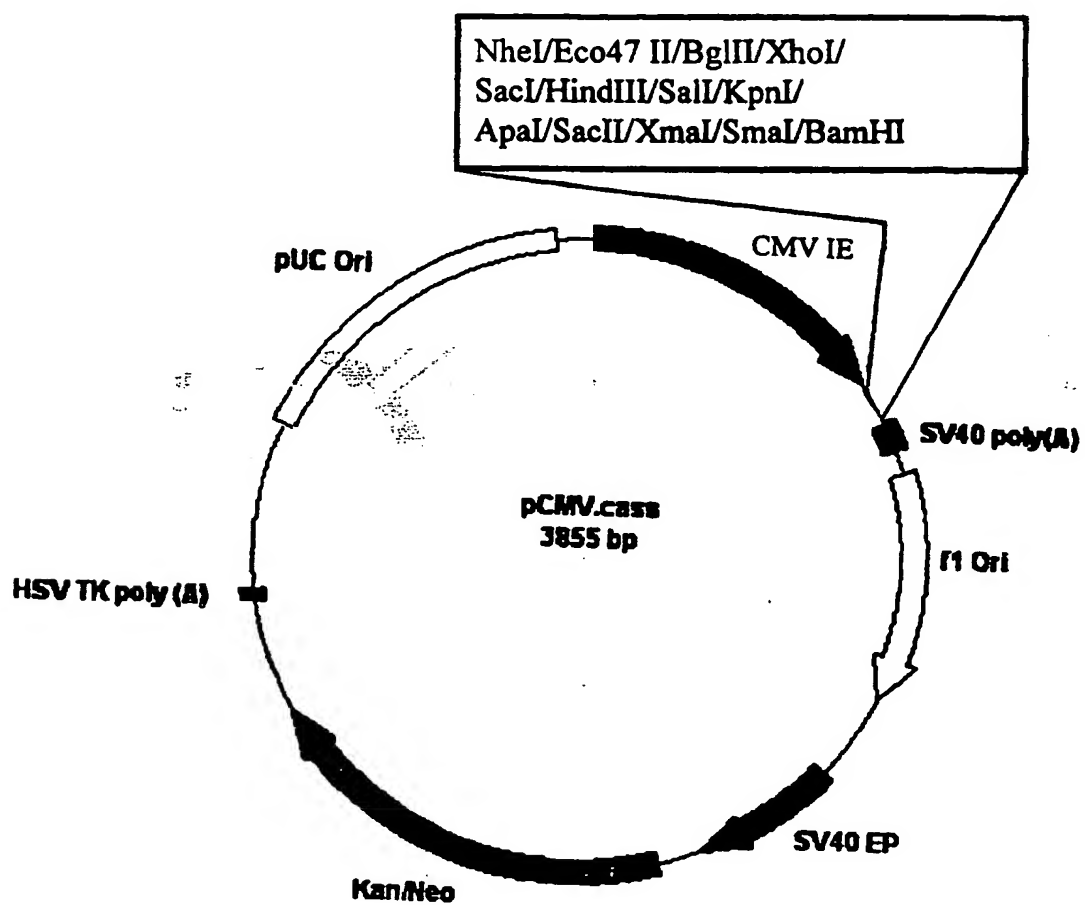


FIGURE 2

3/28

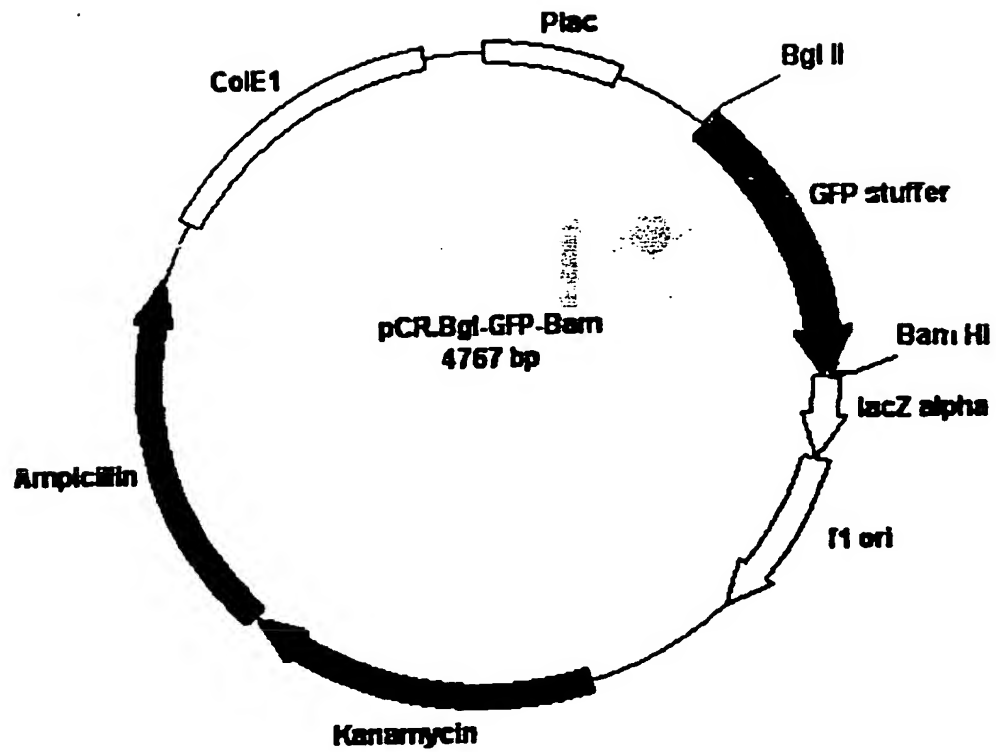


FIGURE 3

4/28

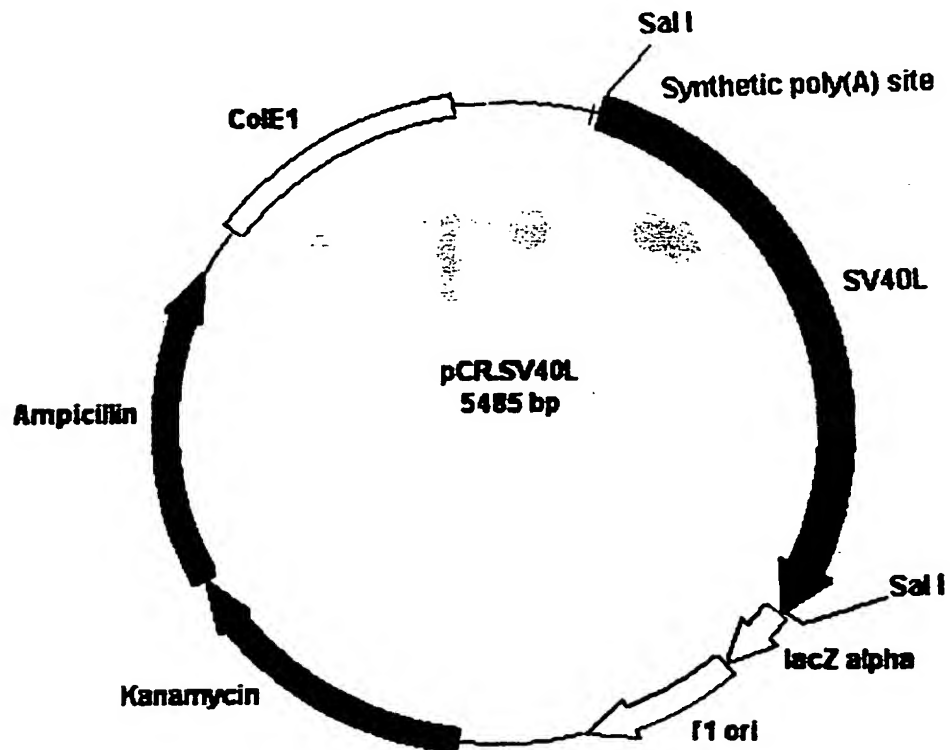


FIGURE 4

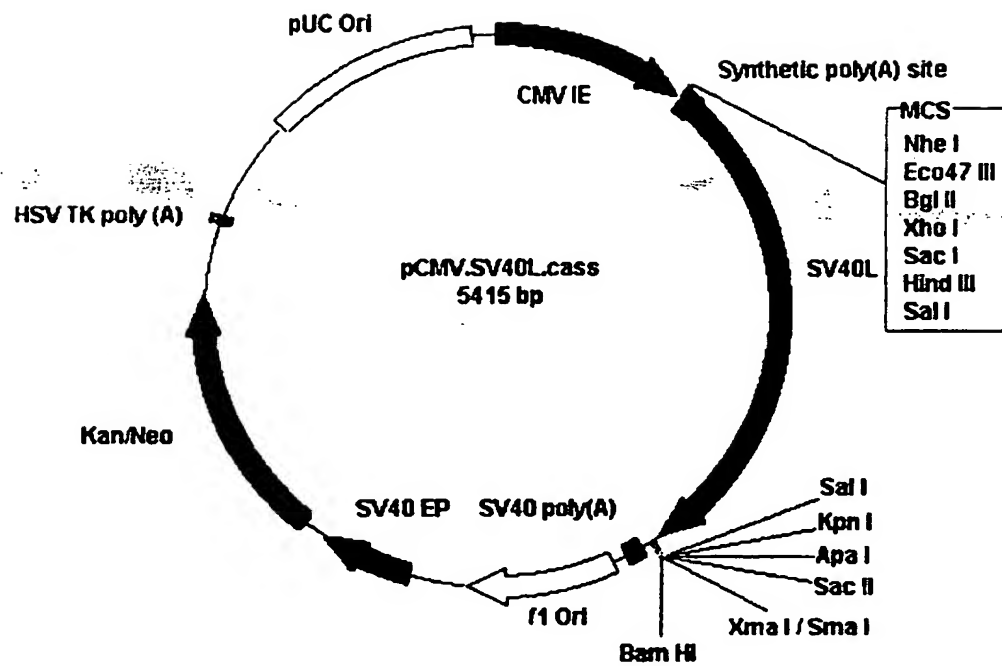


FIGURE 5

6/28

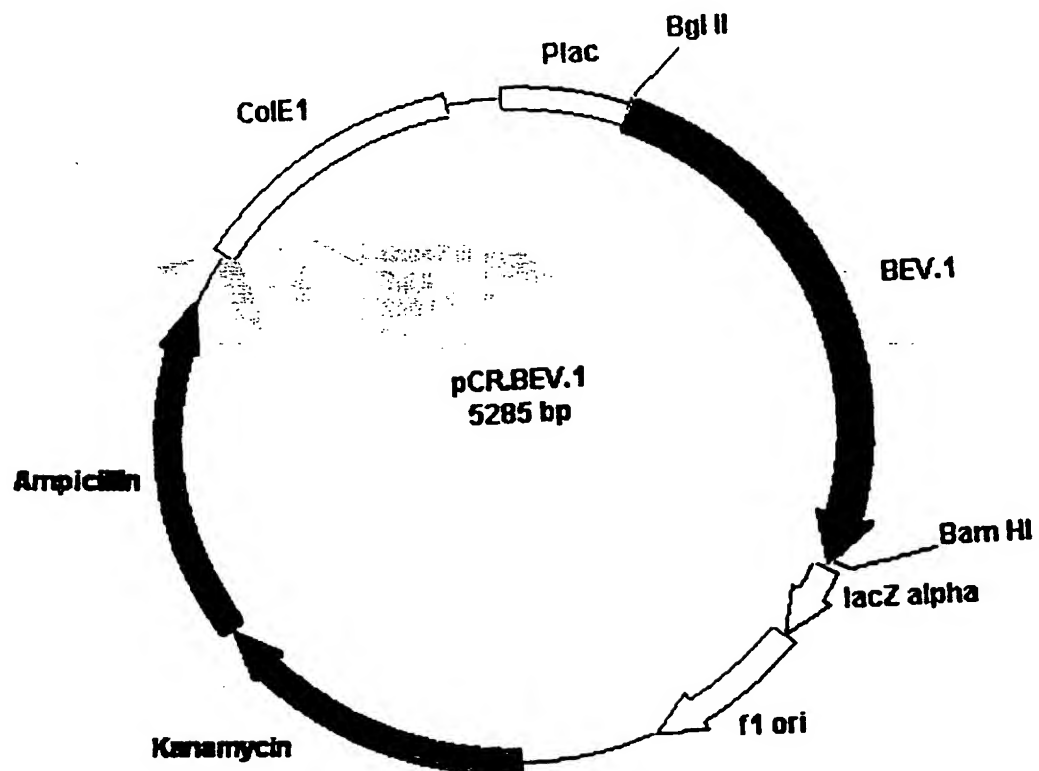


FIGURE 6

7/28

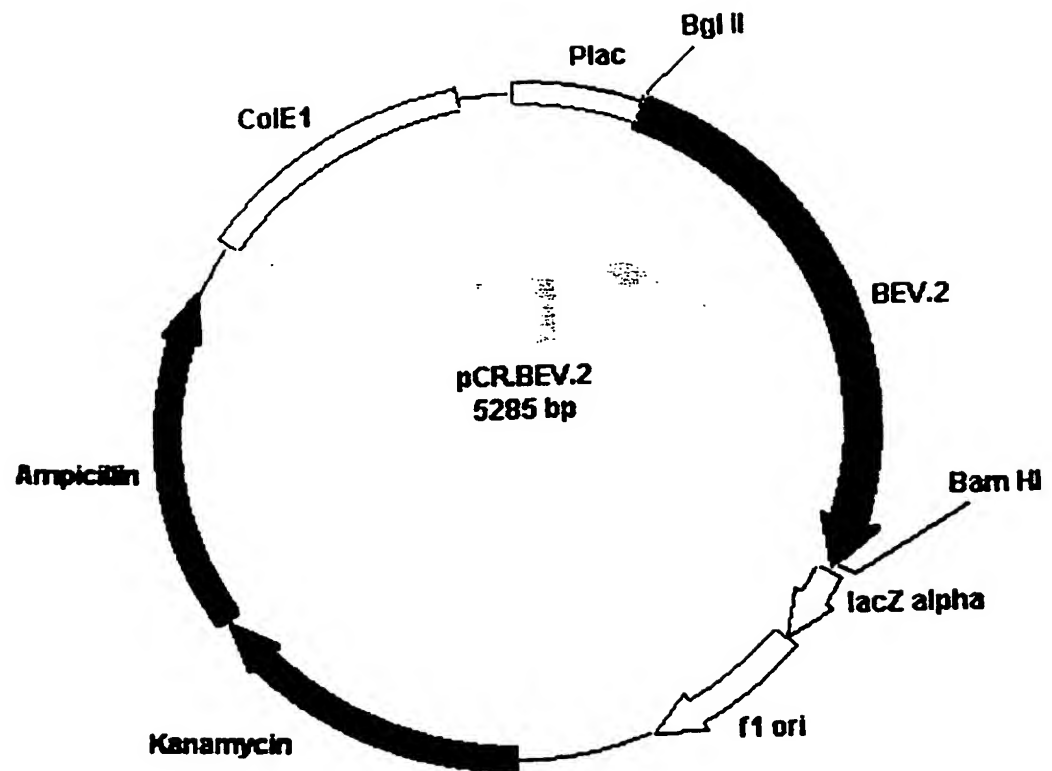


FIGURE 7

8/28

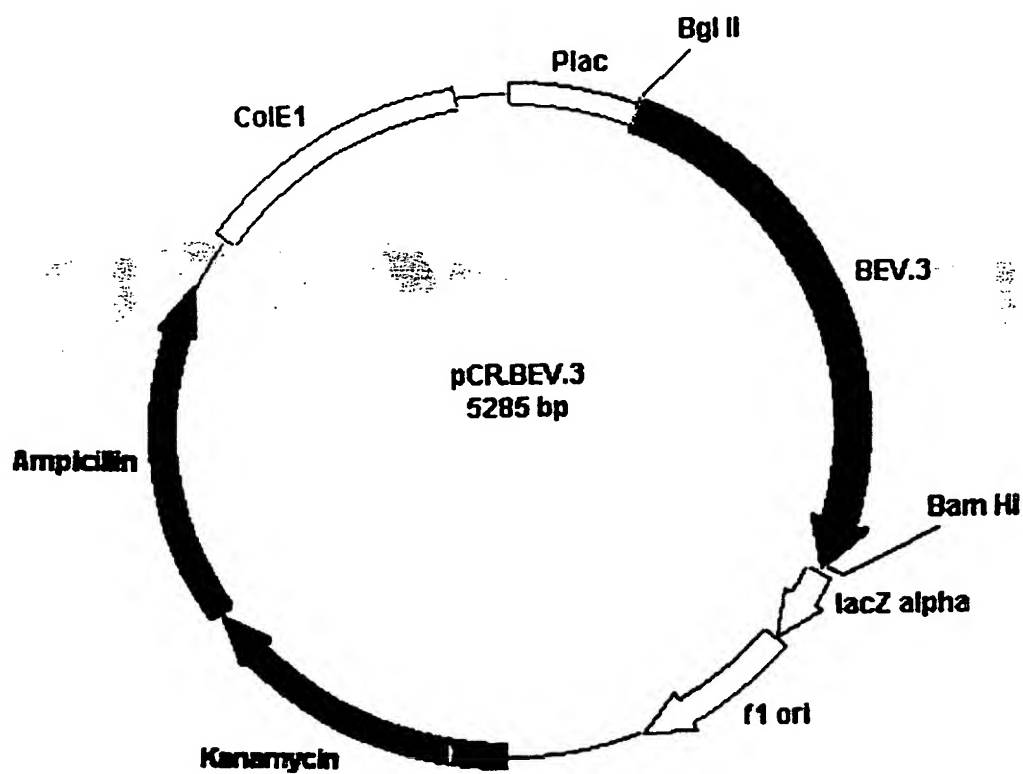


FIGURE 8

9/28

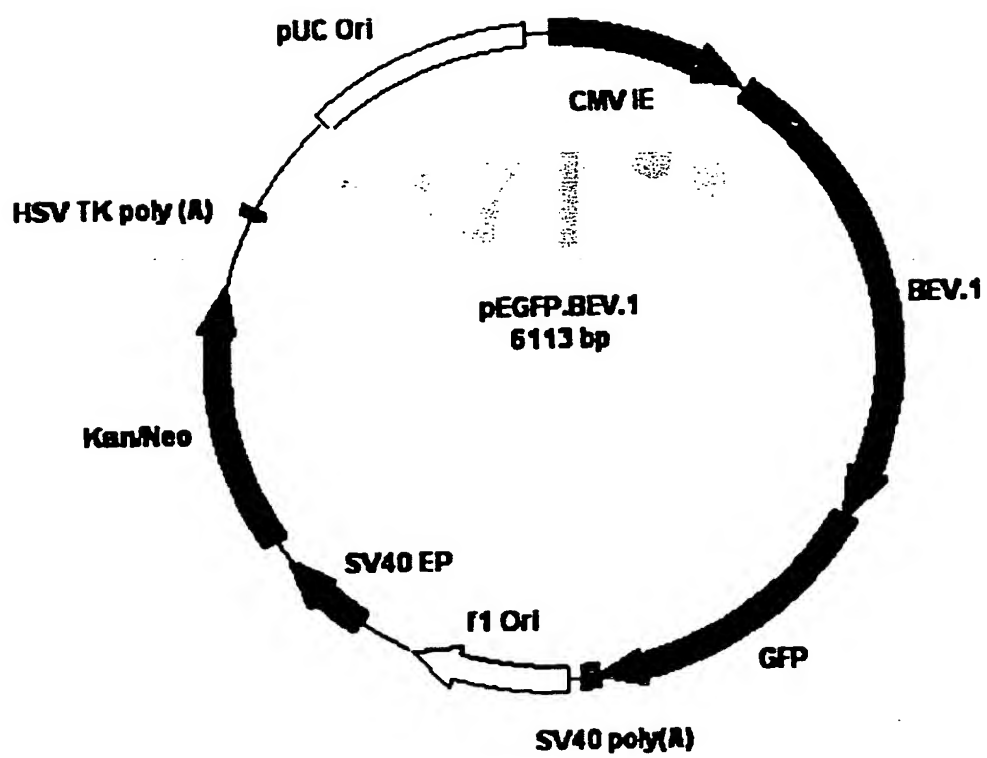


FIGURE 9

10/28

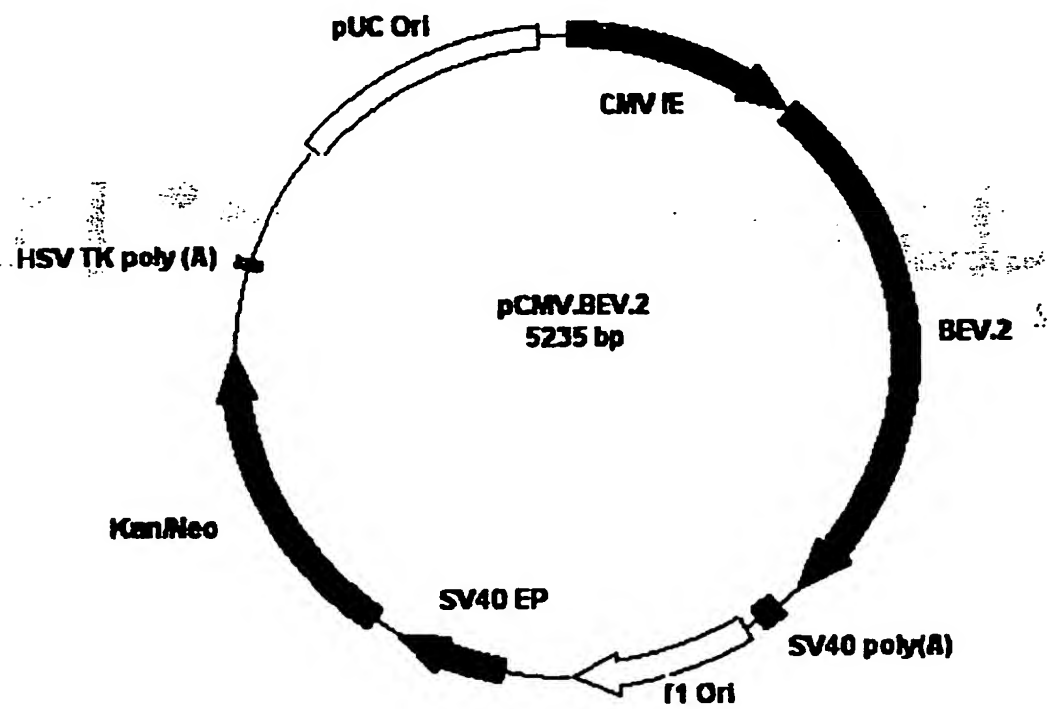


FIGURE 10

11/28

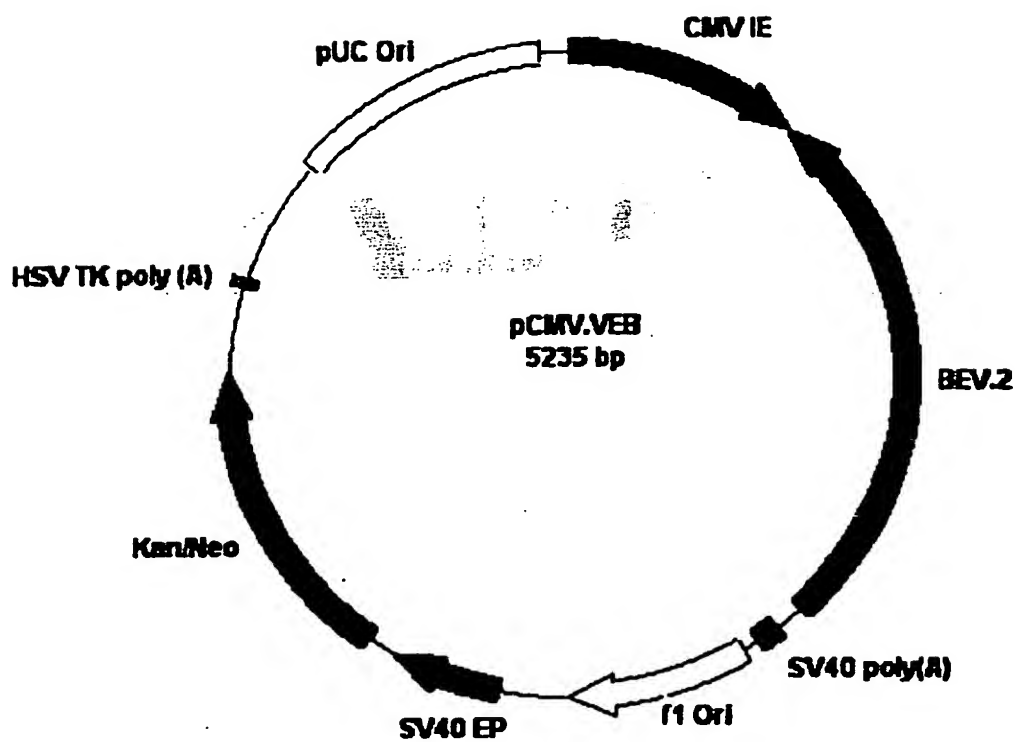


FIGURE 11

12/28

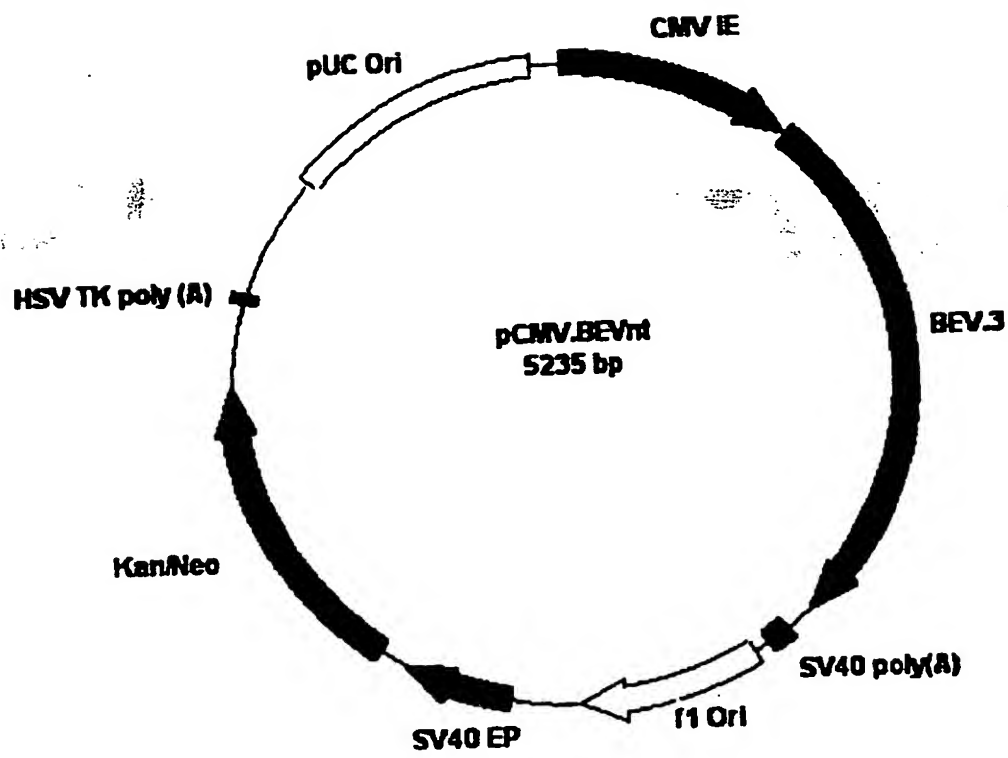


FIGURE 12

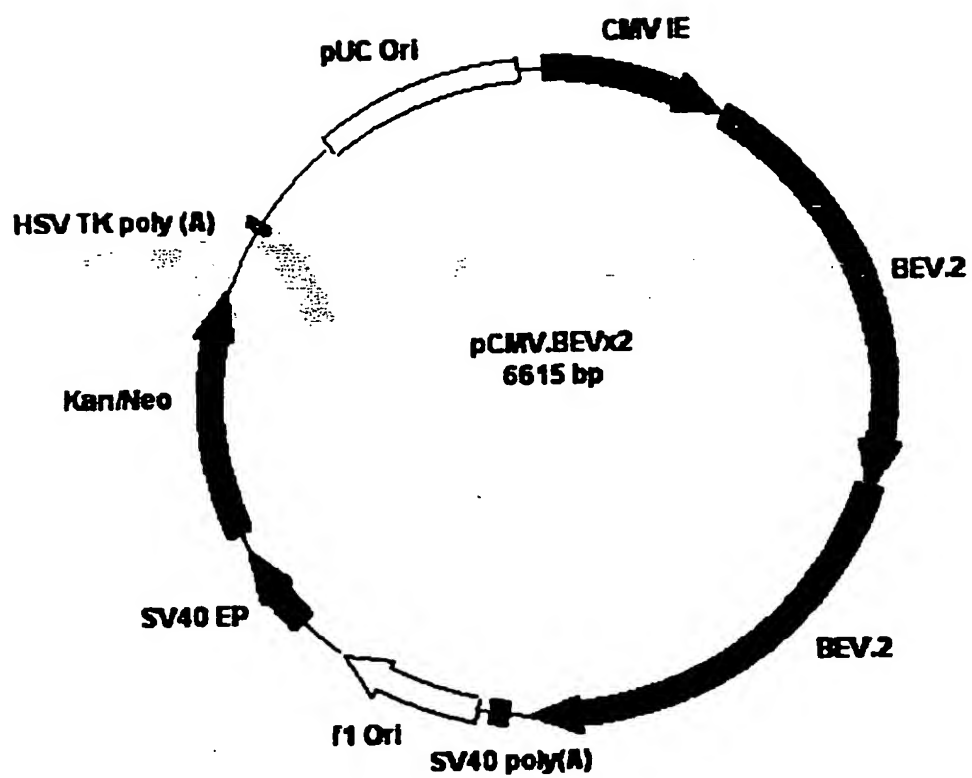


FIGURE 13

14/28

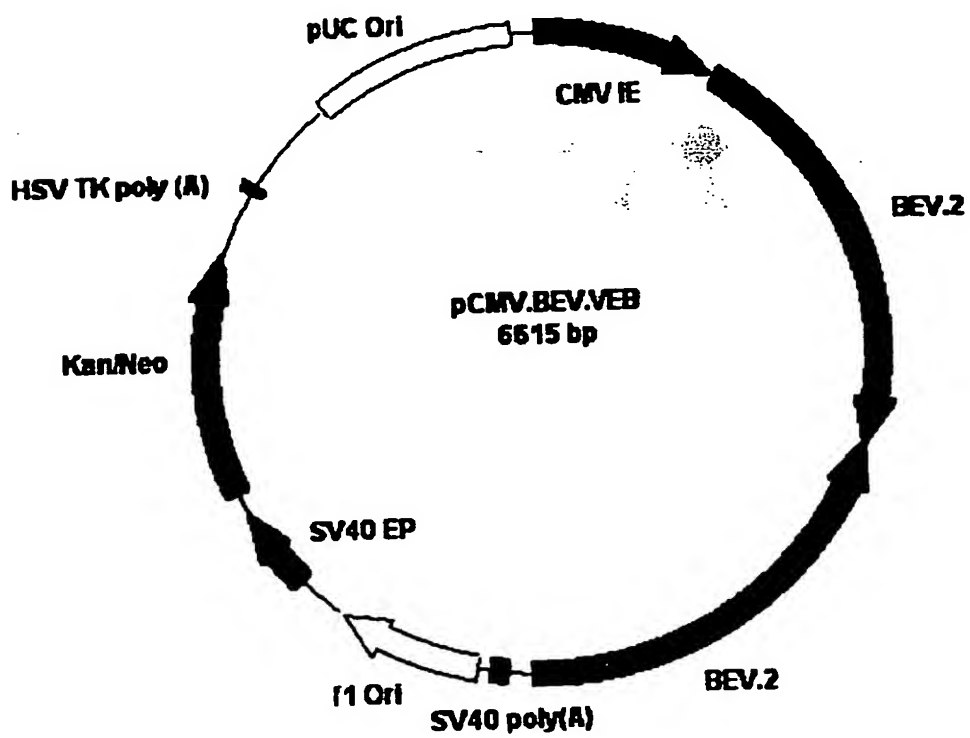


FIGURE 14

15/28

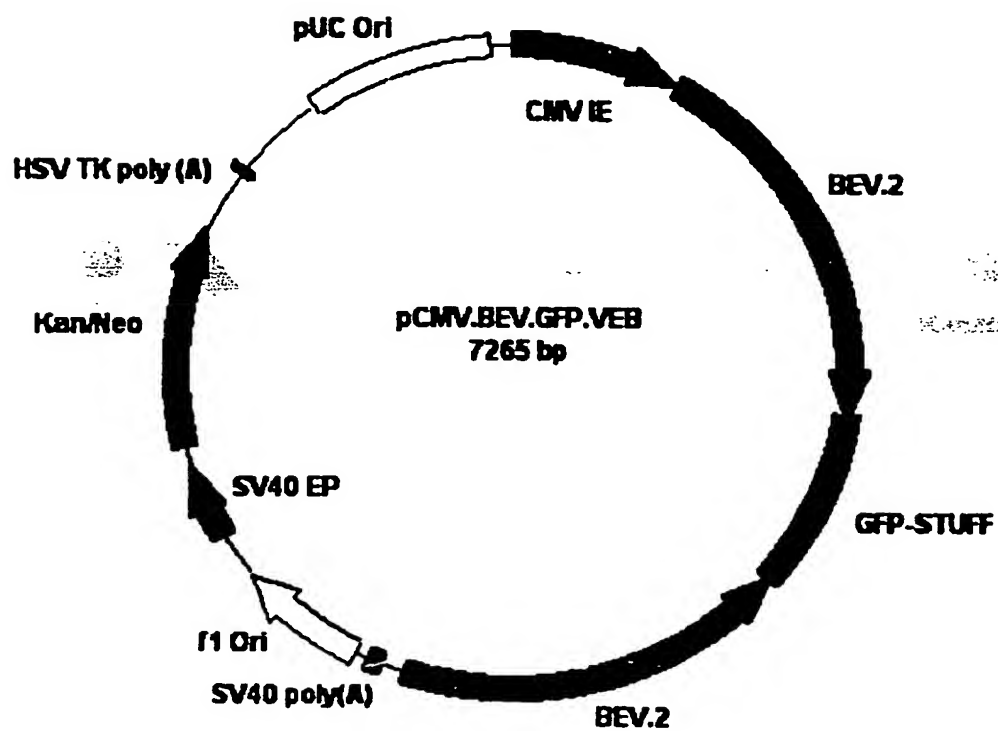


FIGURE 15

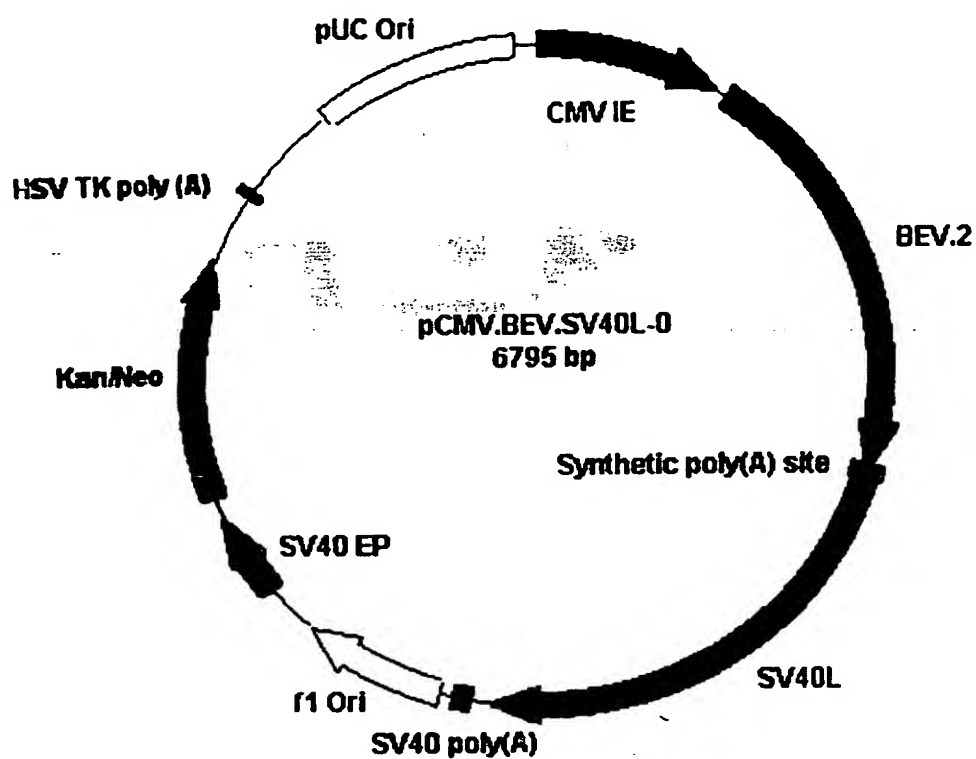


FIGURE 16

17/28

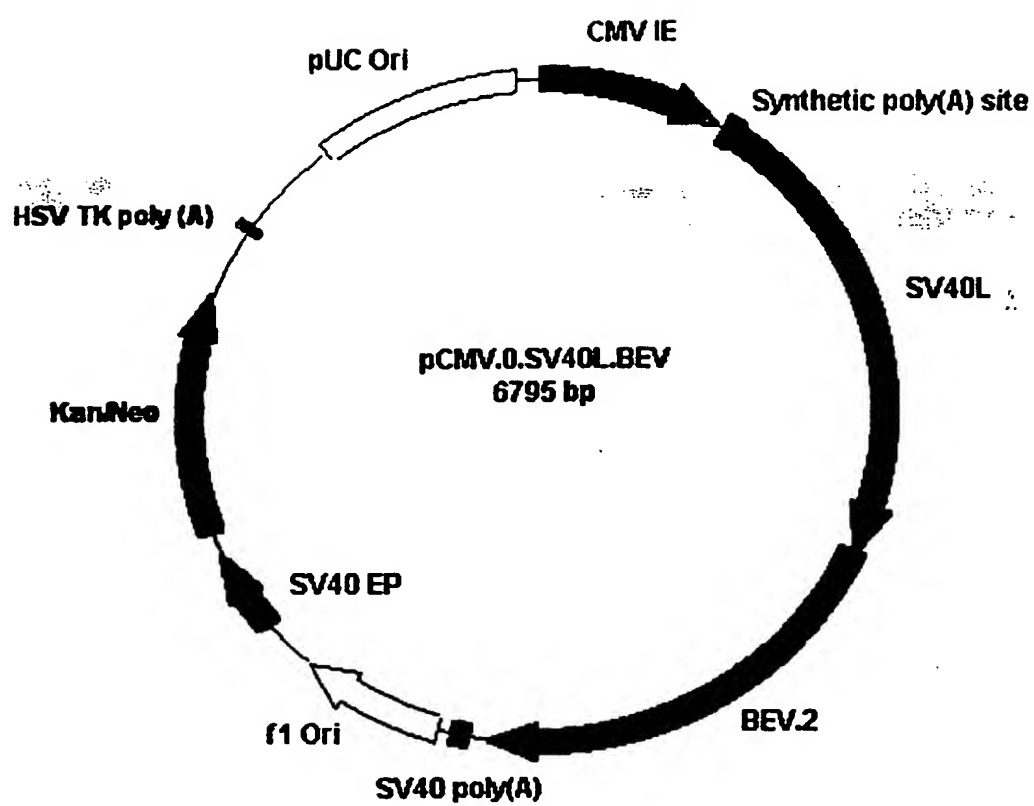


FIGURE 17

18/28

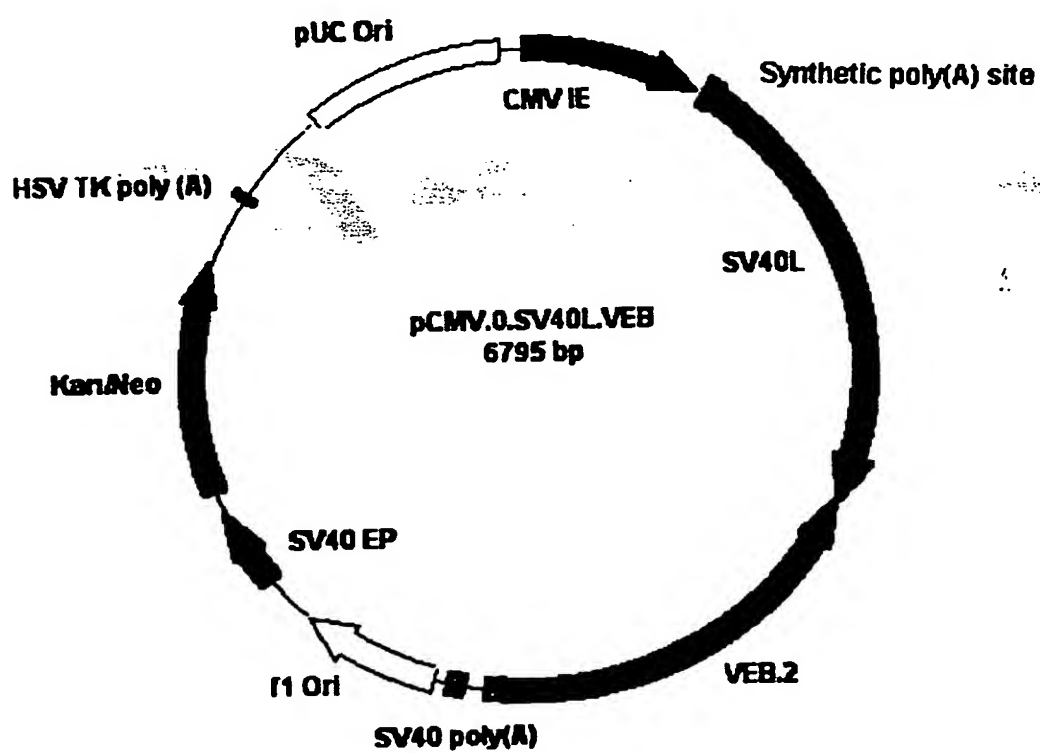


FIGURE 18

19/28

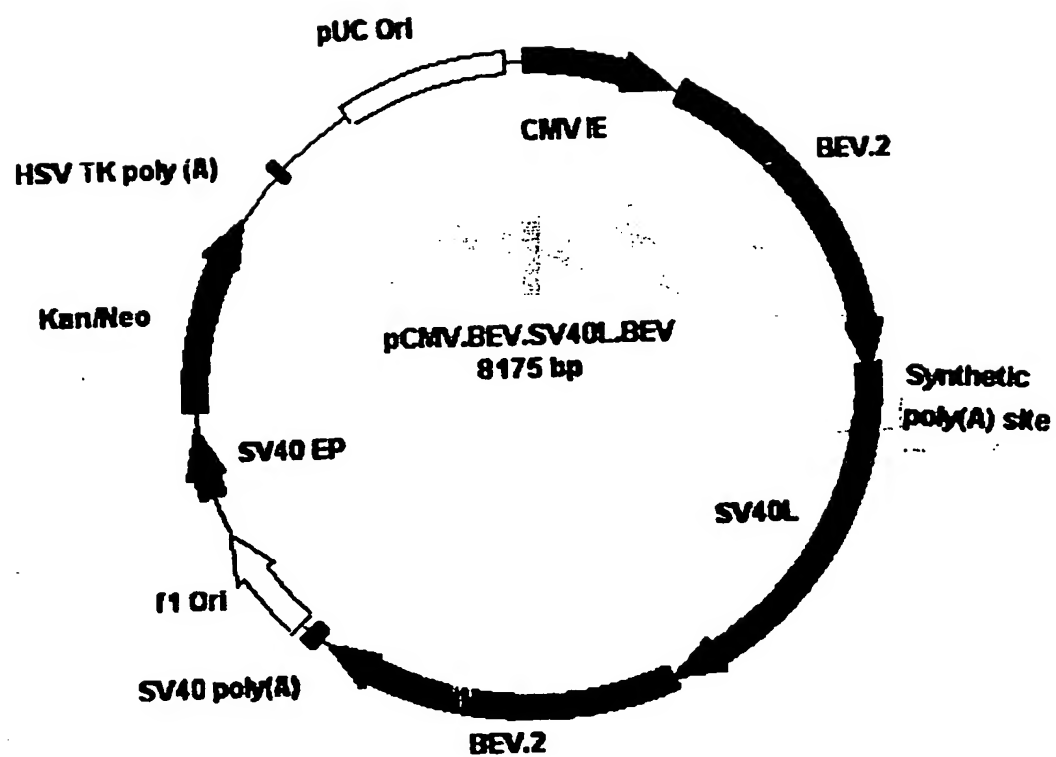


FIGURE 19

20/28

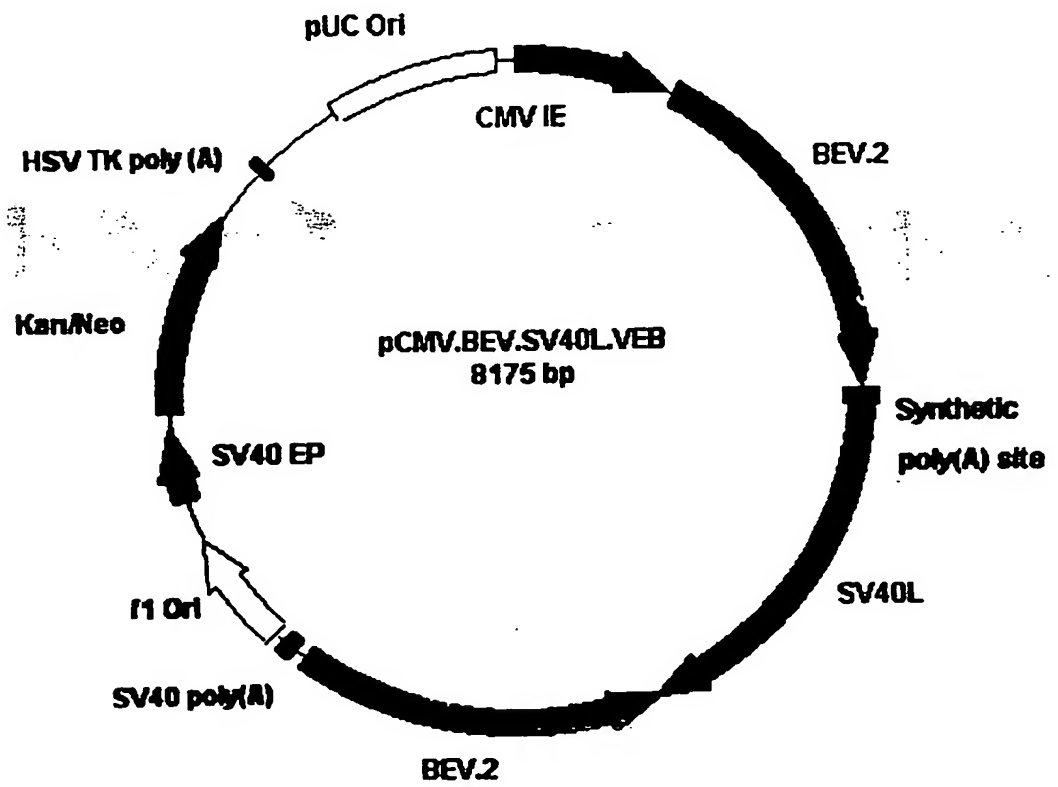


FIGURE 20

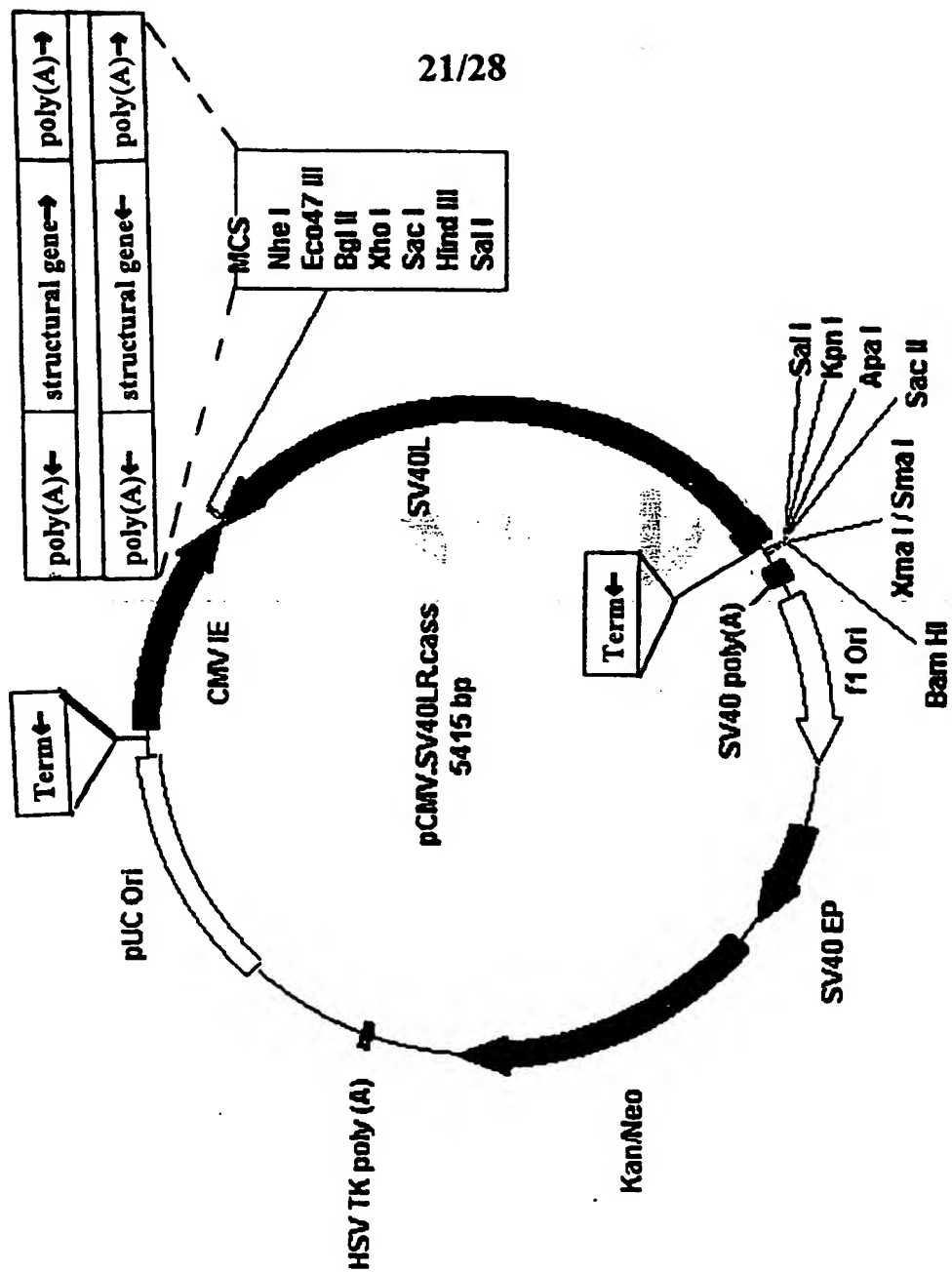


FIGURE 21

22/28

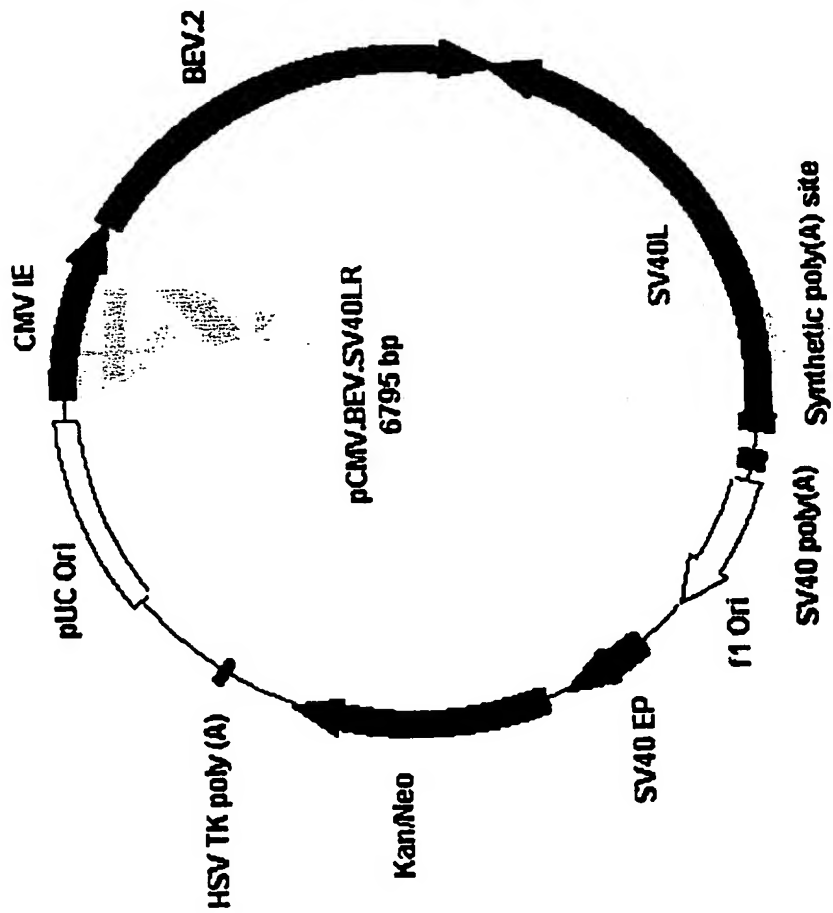


FIGURE 22

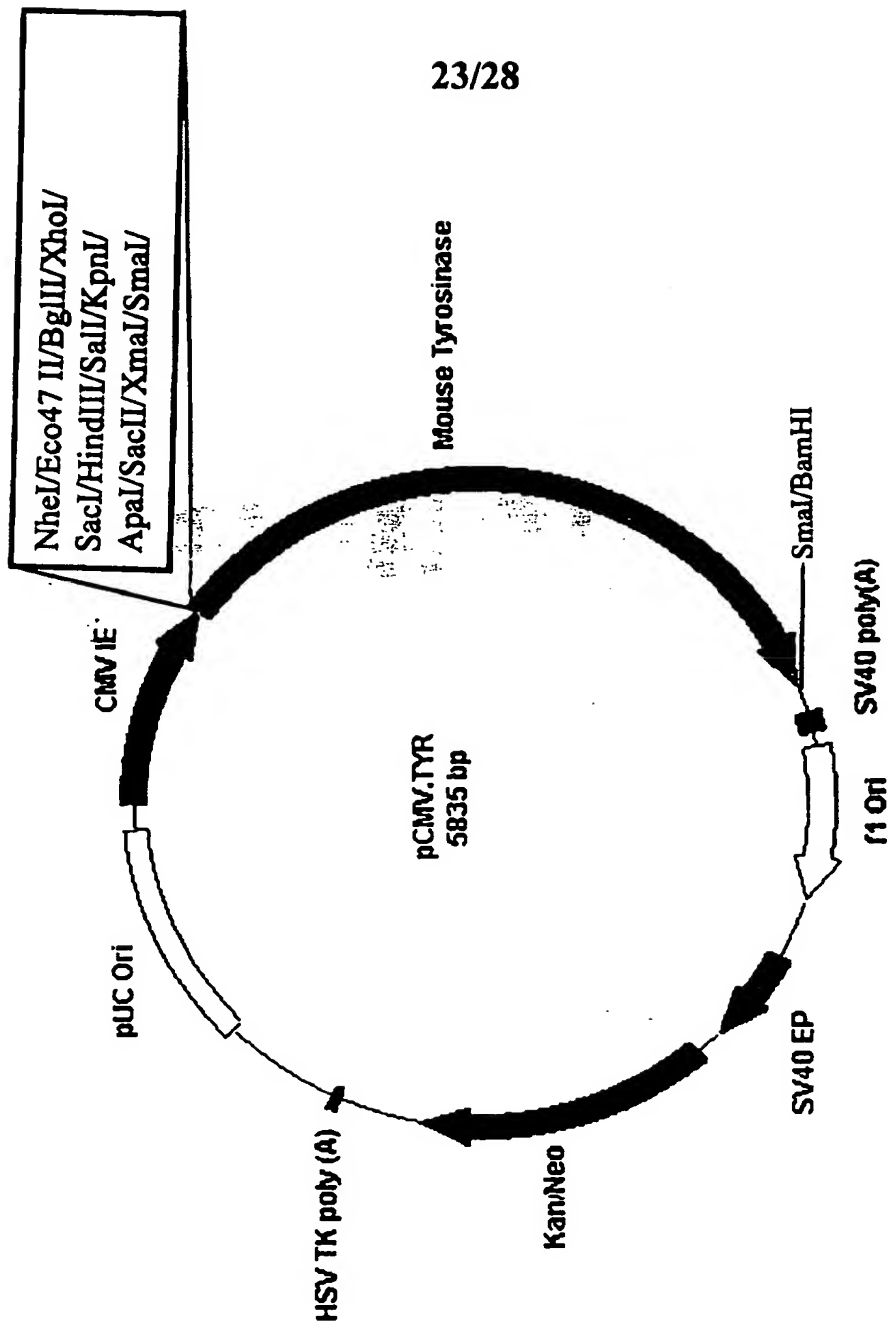


FIGURE 23

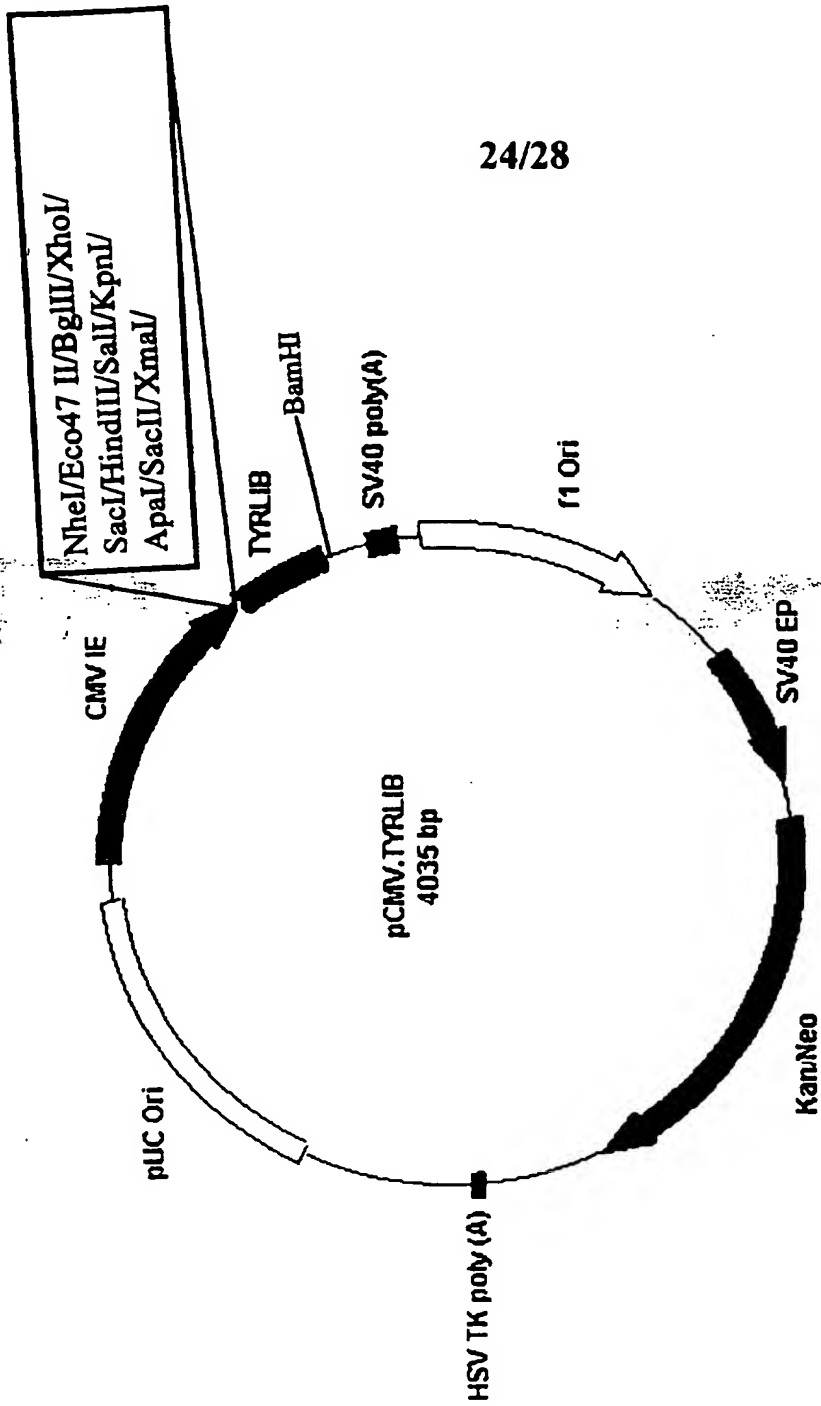


FIGURE 24

25/28

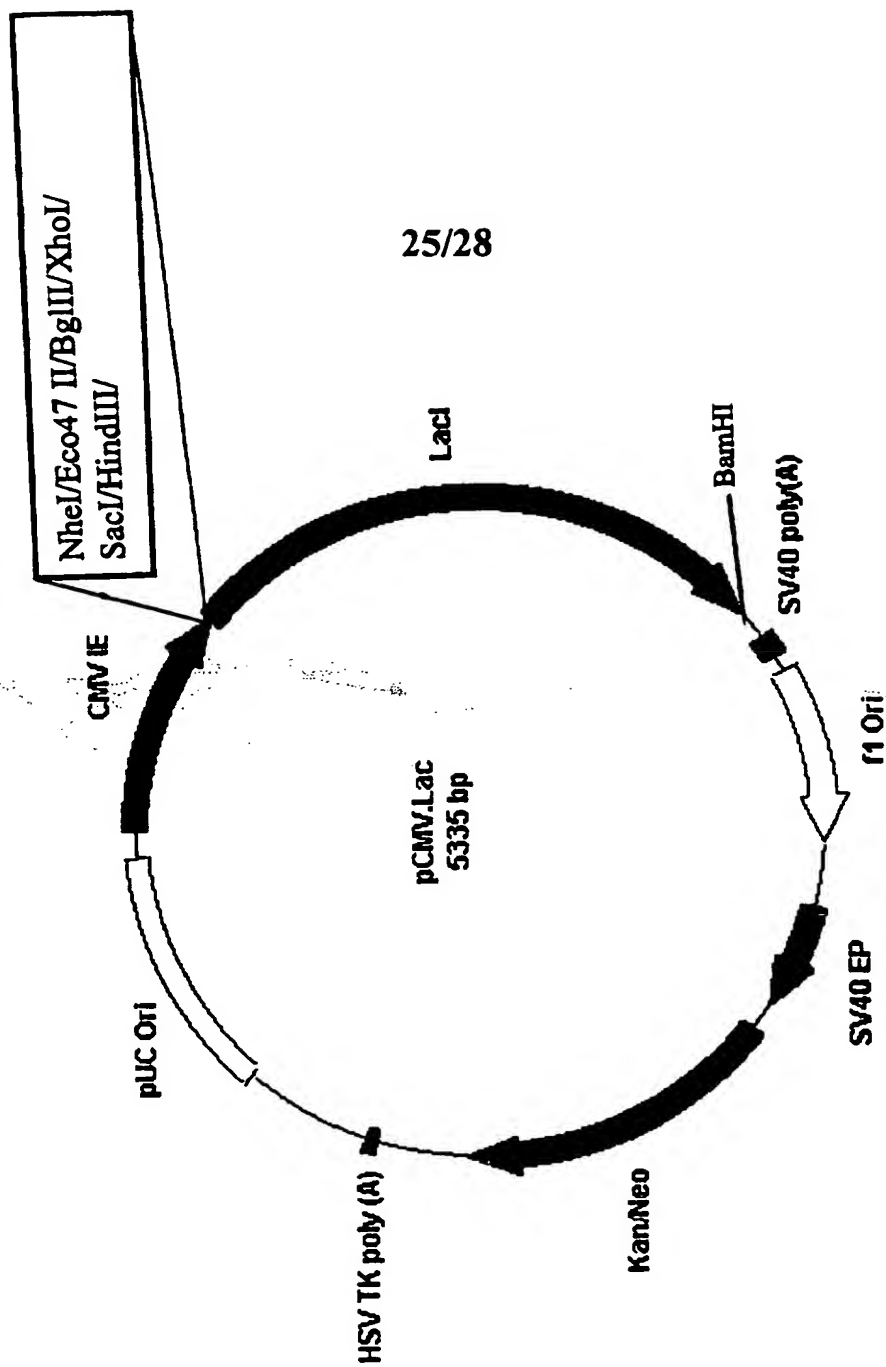


FIGURE 25

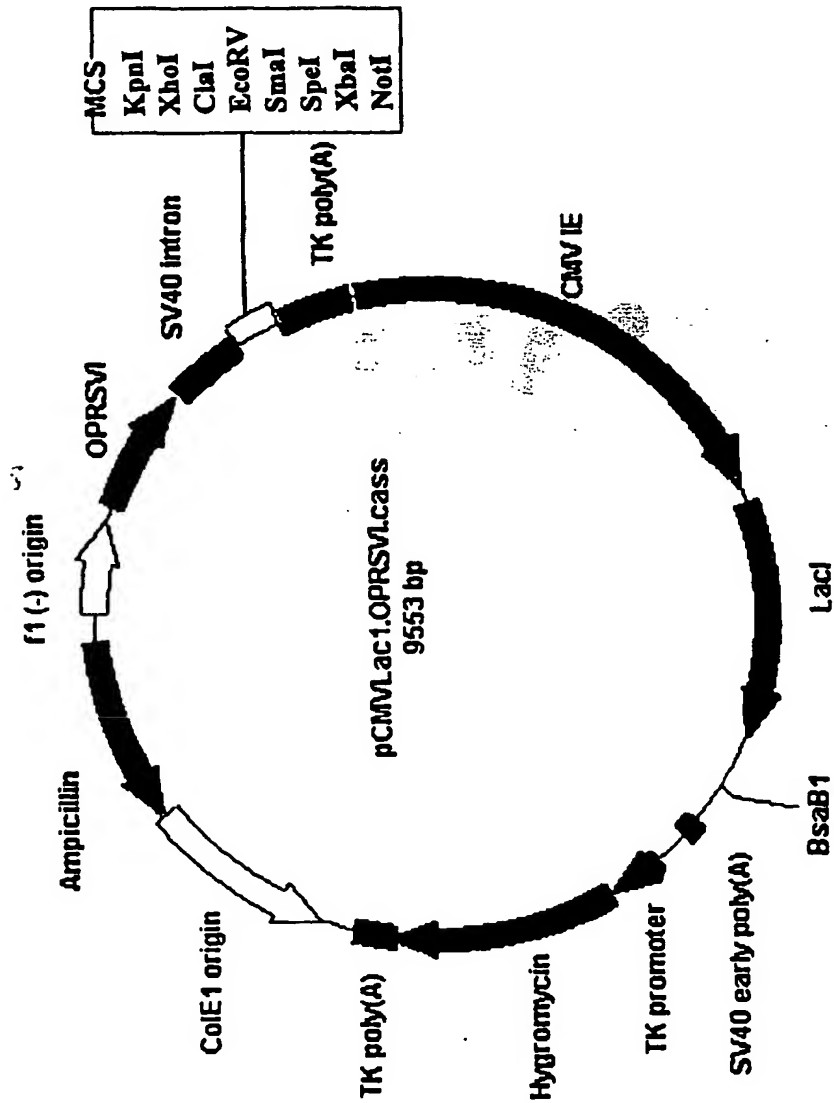


FIGURE 26

27/28

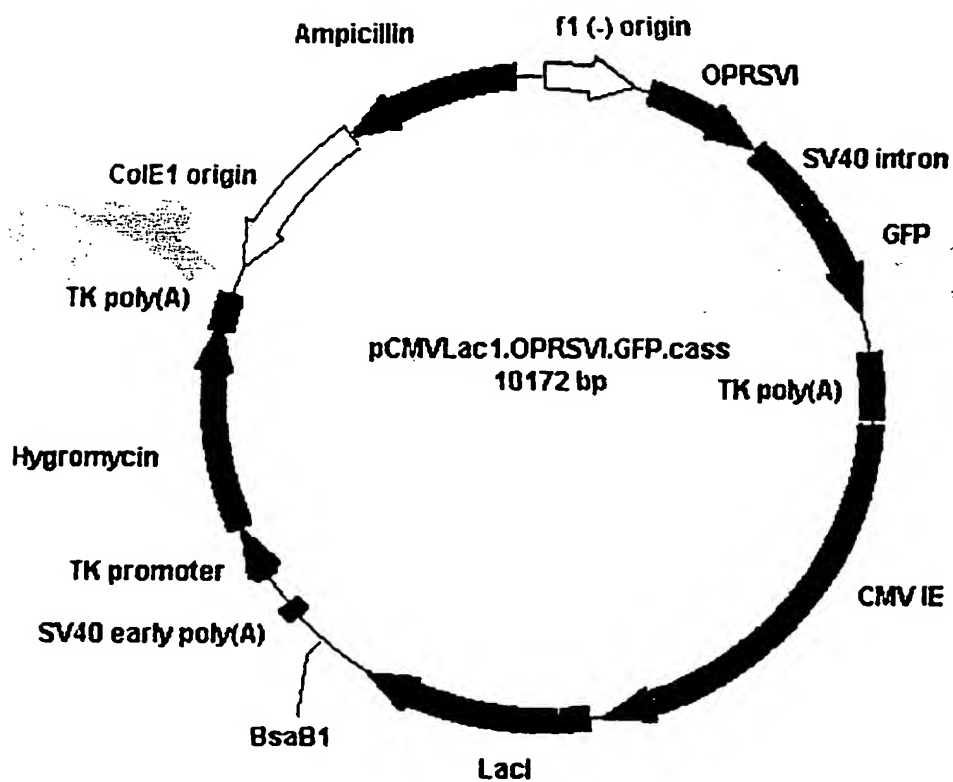


FIGURE 27

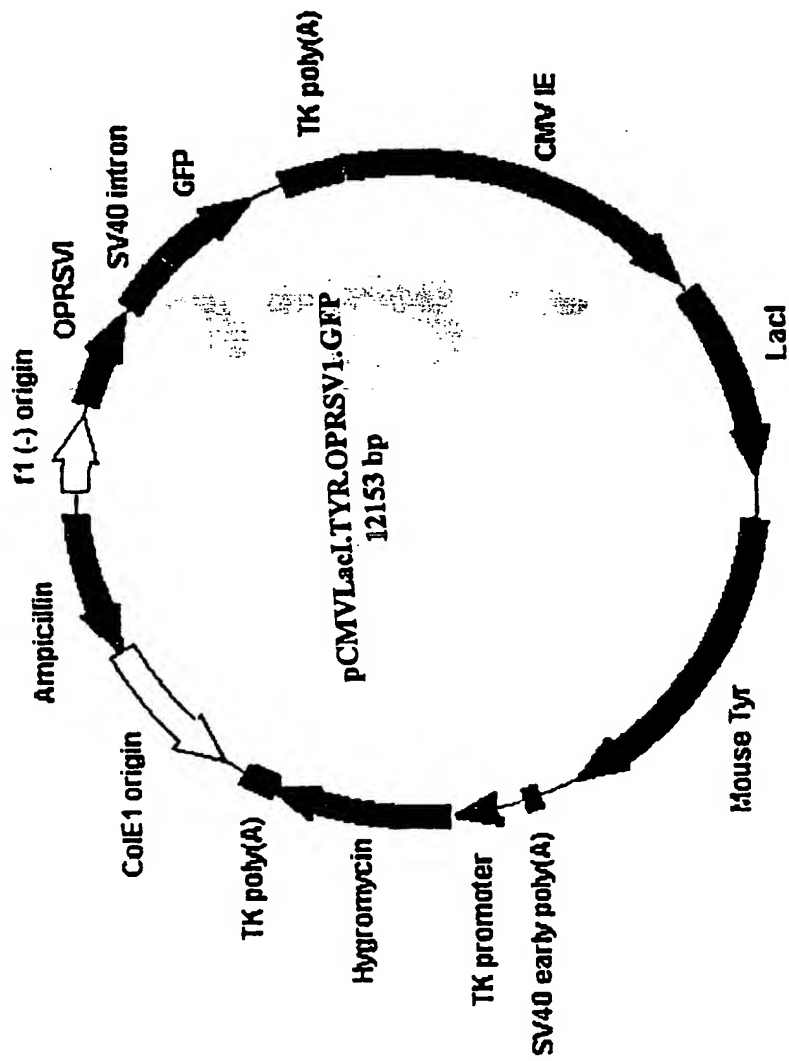


FIGURE 28

